Single chain Fv pr Lead binding MAb 1 Heavy chain amino MaE13 heavy chain. Fv (TU27). Homo sa Interleukin-6 spec Variable region an Variable region an Variable region an Variable heavy sub Antibody 24-31 hum Murine wild-type a Sequence encoded b Heavy chain of 58. Variable region an Sequence of the mo Humanised antibody SH7 single chain a Monoclonal antibod Mouse VH group I(A Wariable heavy chain a Wariable heavy chain a Wonoclonal antibod Mouse VH group I(A Wariable heavy chain a Monoclonal antibod Mouse VH group I(A

Antibody 5H7 heavy Sequence of a chim Variable domain of Whomain of antibo Monoclonal antibod Monoclonal antibod

Variable heavy sub Antibody 24-31 hum G28.5 sFv protein. BD1-G28.5 fusion g Humanised antibody

Title: Perfect score:

Sequence:

protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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Human, antibody, interleukin-6, receptor, IL-6R, light chain, L, H, heavy chain, variable region, mouse, monoclonal; hybridoma; PM1; plasmid, pPM-k3; pPM-h1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1..18
/note=_"Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19..137
/note= "Mature peptide"
                                                                                                                                                                                                                                                                                                          AAY95776
AAR24721
AAW39809
AAR07318
                                                                                                                                                                     ABG98318
AAR24722
AAR63118
                                                                                                                                                                                                                                                                                  AAW00829
AAW19015
                                                                                                                                                                                                                                                                                                                                                                       AAR99875
AAB36827
                                                                                                                                              AAW21937
AAY05267
                                                                                                                                                                                                                                  ABP58448
AAY95781
                                                                                                                                                                                                                                                          AAR64201
AAY94391
                                                                                                                                                                                                                                                                                                                                                            AAW14486
                                                                                                                                                                                                          ABB98908
                                                                                                                                                                                                                       AAR48617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR28671 standard; Protein; 137 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92WO-JP00544
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(first entry)
pPM-hl protein product.
                                                                                                                                                                                 WO9219759-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-APR-1991;
19-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAR-2003
30-MAR-1993
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Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR28671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR2867
 Murine 5B3 antibod
MAD 1.4 heavy chai
Monoclonal antibod
pUC-RVh-PM1f. Syn
pUC-RVh-PM1f. Syn
Single chain Fv pr
Single chain Fv pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pPM-hl protein pro
Antibody 806 varia
                                                                                , Search time 61.7538 Seconds (without alignments) 352.133 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                       A Geneseq 19Jun03:*

| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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| SIDSI/gc
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                                                                                                                                              718
1 MRVLILLWLFTAFPGILSDV......LARTTAMDYWGQGTSVTVSS
                                                                                                                                                                                                                                                1107863
           GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                      1107863 segs, 158726573 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                           protein search, using sw model
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ABB82796
AAB15672
AAW01144
AAW44169
AAR29012
AAR29014
AAY55075
                                                                                   October 22, 2003, 22:03:25
                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
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136
138
138
260
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Match 1
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82.7
81.9
78.3
74.9
74.9
74.8
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718 593.5 583.5 562.5 562.5 538 538 537

426459789

Score

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Result

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The invention relates to an isolated specific binding member (I) which recognizes an epidermal growth factor receptor (EGFR) epitope which is recognizes an epidermal growth factor receptor (EGFR) epitope which is found in tumourigenic, hyperpoliferative or abnormal cells and not detectable in normal cells. The EGFR epitope is located within the region acid sequence alterations or substitutions. From normal EGFR. (I) is capable of binding the de-7 EGFR at an epitope distinct from the interpretations or substitutions. From normal EGFR. (I) is capable of aberrant expression, or in the absence of amplification of normal wild-type gene. The binding member comprises the VH and VL corpspetide sequence of monoclonal antibody (mAb) 806. (I) is useful for creating or diagnosing human or animal body, especially for treating curreating or diagnosing human or animal body, especially for treating curreating cancer which is located in or adjacent the CFR is measured by contacting a biological sample from a mammal: (I) is also useful for detecting the presence of amplified EGFR, de-7 EGFR with high mannose glycosylation is suspected with (I) under conditions that allow binding the presence of amplified EGFR, from the sample and the antibody, where the CFR to the antibody to occur, and detecting cancer in mammals by detecting the presence or activity of an EGFR with indicates the comprising (I), and optionally webicle, carrier or diluent is useful for detecting cancer in mammals, especially for treating brain-resident cancers that produce aberrantly expressed EGFR in mammals, and malignant mammals, and malignant mammals, and malignant mammals, and malignant constructions agrrowless or requence or activity of merreal tumours in mammals. The present sequence represents the mamble mammals and malignant and malignant is an expected agrrowless the mammals. The presents requence represents the presence or activity of a medicate agrrowlessed EGFR in mammals. The present sequence represents the mamble mammals. The present sequence repr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GNKLEWMGYISYSGNTRYNPSLKSRISITRDTSKNOFFLQLNSVTIEDTATYYC---VTA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GNKLEWMGYISYSGITTYNPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel specific binding members, particularly antibodies recognizing epidermal growth factor receptor epitope found only in tumorigenic cells, useful for diagnosing, preventing and treating cancer in mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MRVLILLWLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFP
       Scott AM, Renner C, Ritter
.ns P, Cavenee WK, Huang H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 24; Length 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 82.7%; Score 593.5; DB 24; Length Best Local Similarity 83.9%; Pred. No. 1.8e-46; Matches 115; Conservative 5; Mismatches 14; Indels
          is C, Scott
Collins P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ź
                                                                                                                                                                                                                                                                                                          Claim 6; Fig 14B; 123pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 TTAMDYWGQGTSVTVSS 137
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          Panousis
                                    Stockert E,
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Jld LJ, Johns ...
Jungbluth A, Stockert
                                                                                                            WPI; 2003-129282/12.
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                                                                                                                                   N-PSDB: ABZ23940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                               The sequences given in AAR28670-71 were encoded by plasmids which were used in example to illustrate the production of a human antibody which recognises human interleukin-6 receptor (IL-6R). The antibody which comprises light (L) chain and heavy (H) chain variable regions which were derived from a mouse monoclonal antibody produced from the hybridoma PM1 which contained the plasmids PPM-k3 and pPM-h1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GNKLEWMGYISYSGITTYNPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MRVLILLMLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFP
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                                                                                                                                                                                 Reconstituted human antibody to human interleukin-6 receptor - has low antigenicity and contains mouse V-region complementarity determining regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 718; DB 13; Length 137; 100.0%; Pred. No. 8.7e-58; cive 0; Mismatches 0; Indels 0
                                                             Tsuchiya M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibody 806 variable heavy chain (VH) region.
                                                           Saldanha JW, Sato K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "mAb 806 VH region"
                                                                                                                                                                                                                                                                                   Disclosure; Page 122-123; 207pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1..18
/note= "signal peptide"
19..134
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28-SEP-2001; 2001US-326019P.
21-DEC-2001; 2001US-342258P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 137; Conservative
          (CHUS ) CHUGAI SEIYAKU
                                                        Bendig MM, Jones ST,
                                                                                                         WPI; 1992-398882/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137 AA;
                                                                                                                                   N-PSDB; AAQ30756
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RESULT 2 ABB82796

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Peptide Protein

Key

Gaps

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16-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                          Kawauchi Y, Masuho Y,
                                                                                                                                                                                                                                                                                                                                                                            1996-333946/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 AA;
                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAT40804
                                                                                                                                                                                                                                       27-DEC-1995;
 Mus musculus
                                                   Binding-site
                                                                                 Binding-site
                                                                                                                  Binding-site
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                                                                                                                                                                                                                                                                         29-DEC-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is the heavy chain variable region of 5B3 antibody. The cDNA encoding this sequence was obtained from total RNA extracted from a SB3 hybridoma by RT-PCR. 5B3 is an igg1 antibody derived from a TNP-KLH immunised mouse. Its binding to TNP or DNS antigen can be blocked by very low amounts of TNT and it can therefore be used in a method for detecting small assayed explosive molecules. Molecules are detected using a piezoelectric semunoassaying in liquid phase allows stationary and flow analysis of an aqueous sample. The method is sufficiently sensitive for detection of low molecular weight molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GNKLEWMGYISYSGITTYNPSLKSRISITRDTSKNOFFLOLNSVTTGDTSTYYCARSLAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GNKLEWMGYISYSGFISYNPSLRSFIRFTRDISKNOFFLQLNSVISEDTATYYCARWDYG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monoclonal antibody; phospholipase; myocardial infarction; panoreatitis; cerebral infarction; acute kidney failure; colitis; chronic rheumatism; adult respiratory distress syndrome; cardiac shock; treatment; preclinical testing; disease; hybridoma
                                               Mouse; 5B3 antibody; IgG1; piezoelectric immunoassay;
small molecule explosive detection; 2,4,6-trinitrotoluene; TNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAb 1.4 heavy chain, directed against type II phospholipase A2
                                                                                                                                                                                                                                                                                                                                                                                                            Apparatus for detecting small molecules, especially explosives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.9%; Score 588; DB 21; Length 136;
83.8%; Pred. No. 5.8e-46;
ive 8; Mismatches 12; Indels
              Murine 5B3 antibody heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                               comprises a piezoelectric crystal -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW01144 standard; Protein; 136 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 3A; 90pp; English
                                                                                                                                                                                                                                                                     (YISS ) YISSUM RES & DEV CO. (YEDA ) YEDA RES & DEV CO LTD.
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                                                                                                                                                                                                                                       99IL-0128212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                       Willner I, Eshhar Z;
                                                                                                                                                                                                                                                                                                                                                          2000-524259/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 AA;
                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-524259/
N-PSDB; AAA74604.
                                                                                                                                  WO200043774-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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GNKLEWMGYISYSGITTYNPSLKSRISITRDTSKNOFFLQLNSVTTGDTSTYYCARSLAR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MRVLILLWLFTAFPGFLSDVQLQESGPGLVKPSQSLSLTCMVTGYSITSDYAWNWIRQFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful in the treatment of myocardial infarction, cerebral infarction, acute kidney failure, chronic rheumatism, cardiac shock, parcetaitis, adult respiratory distress syndrome and collitis. The antibodies were generated by immunising Balb/C mice with recombinant human type II phospholipase A2. Spleen cells from the mice were fused with mouse myeloma P3U1 (P3x63Ag8·U1) and the hybridomas obtained were screened for phospholipase A2 inhibitory activity. Active clones were isolated including 12Hs, 1.4 and 10.1. These were cultured and the antibody isolated from the culture supernatoral by precipitation with ammonium sulphate and purification on a column of protein A sepharose CL4B. Because the antibody acts on the primate and mouse forms of enzyme as well as human it is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Monoclonal antibody 1.4 heavy chain against type II phospholipase A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monoclonal antibody inhibiting type II phospholipase A2 activity for treatment of myocardial and cerebral infarction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monoclonal antibodies which inhibit type II phospholipase A2 are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 17; Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yasunaga T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             particularly suitable for preclinical testing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Takasaki J,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; Figure 11; 69pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (YAMA ) YAMANOUCHI PHARM CO LTD
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                                  49..54
/label= CDR 1
69..84
/label= CDR 2
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/label= CDR
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25-APR-1991;
19-FEB-1992;
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                                             pUC-RVh-PM1f
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25-MAR-2003
30-MAR-1993
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                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                         Region
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                                                                                                                                                                              Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents the monoclonal antibody 1.4 heavy chain against type II phospholipase A2, from the present invention. The present invention of present invention of the present invention of the present invention of the present invention of the present invention of administration of cisplatin for the treatment of cancer. The method comprises treatment with a monoclonal antibody which inhibits the comprises treatment with a monoclonal antibody which inhibits the phospholipase A2 of human origin), or with a protein or peptide possessing the same inhibitory activity and containing a part of the possessing the same inhibitory activity and containing a part of the apendor mouse type II phospholipase A2, and has the ability to release type II phospholipase A2, and has the ability to release type II phospholipase A2 bound to a cell membrane. Three specific monoclonal antibodies having these properties which can be used are 12H5, 10.1 and 1.4, derived from hybridomas FERM BP-5300, FERM BP-529 and FERM BP-529 respectively. The method can be used for suppressing the nephrotoxicity which is a characteristic feature of cisplatin administration, and therefore allowing more efficient use of the part of an anticancer agent, e.g. by allowing an increased dosage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GNKLEWMGYISYSGITTYNPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GNKLERMGYIRYSGYTSYNPSLKSRIFITRDTSQNQFFLHLTSVTTEDTATYYCTRDL-D 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MRVLILLWLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFP
               Monoclonal antibody, type II phospholipase A2, inhibition, cisplatin, amelioration, kidney disorder, nephrotoxicity, anticancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                Amelioration of kidney disorders caused by cisplatin administration - by treatment with an antibody inhibiting type II phospholipase A2 activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 562.5; DB 1
Pred. No. 1.2e-43;
                                                                                                                                                                                                                                                                          Takasaki J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 38; 74pp; Japanese.
                                                                                                                                                                                                                                                                          Masuho Y,
                                                                                                                                                                                                                                        (YAMA ) YAMANOUCHI PHARM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136
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81.0%;
                                                                                                                                                                                         96JP-0247635.
96JP-0167286.
                                                                                                                                                             97WO-JP02241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 78.3
Best Local Similarity 81.0
Matches 111; Conservative
                                                                                                                                                                                                                                                                        Kawauchi Y,
                                                                                                                                                                                                                                                                                                        WPI; 1998-076914/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 AA;
                                                                                                                                                                                                                                                                                                                         N-PSDB; AAV12261
                                                               Unidentified
                                                                                                                                                           27-JUN-1997;
                                                                                             WO9749427-A1
                                                                                                                                                                                           19-SEP-1996;
                                                                                                                                                                                                          27-JUN-1996;
                                                                                                                                                                                                                                                                      Науавһі К,
                                                                                                                             31-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                be used.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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AAR29012
ID AAR2
XX
AC AAR2
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EWMGYISYSGITTYNPSLKSRISITRDTSKNOFFLQLNSVTTGDTSTYYCARSLARTTAM 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                             Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR; complementarity determining region; mouse; monoclonal; hybridoma; plasmid; polymerase chain reaction; amplify.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       has low antigenicity and contains mouse V-region complementarity determining regions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reconstituted human antibody to human interleukin-6 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tsuchiya M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74.9%; Score 538; DB 13; 75.9%; Pred. No. 2.1e-41; live 15; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sato K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 138-9; 207pp; Japanese.
                                                                                                                                                                                                                                                            /note= "Leader peptide"
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                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                         CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                        CDR2
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/label= CDR3
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/label= FR2
                                                                                                                                                                                                                                                                                                                                                                                                                                           86..117
/label= FR3
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/label= FR4
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(updated)
(first entry)
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/label= (
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/label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1992-398882/48;
N-PSDB; AAQ31360.
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Matches 101; Conserv
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AAR29012 standard; Protein; 138 AA.

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ð 셤 8 AAR29012

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Gaps

64 65

125

ò g AAR29014;

AAR29014 RESULT

Synthetic

Peptide

Region Region Region Region

Region

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65 EWMGYISYSGITTYNPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLARTTAM 124
                                                                                                                                                                    This sequence represents a single chain FV (ScFV) sequence.

The invention relates to a method for isolating a gene encoding a membrane-bound protein, comprising introducing a vector into a cell, contacting an antigen with the cell expressing the fused protein encoded by the vector on its surface to select an antigen-binding cell, and isolating the CDNA. The vector contains DNA encoding a secretable functional protein with antigenicity and binding affinity, and a CDNA ligated to DNA downstream of the 3' end of the coding sequence. The method can be used to isolate a membrane-bound protein for diagnosis and study. It can also be used for producing drugs treating abnormal functions of the protein. Such a technique is efficient and selective, which is different from the prior-art transmembrane trap (TWT) method wherein an epitope recognised by an antibody is carried in a fused
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene isolation; membrane-bound protein; fusion protein; drug production; antigen-binding cell; secretable functional protein; antigenic protein; protein isolation; diagnosis; ScFv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      with low or no antigenic binding activity, for diagnosis, study of, and production of drugs treating abnormal functions of the protein
                                                                                               6 ILFLVATATGVHSQVQLQESGPGLVRPSQTLSLTCTVSGYSITSDHAWSWVRQPPGRGL
                                                                          5 ILLWLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Efficient and selective isolation of a gene encoding membrane protein
                                     ö
Length 138;
                                     17; Indels
74.9%; Score 538; DB 13;
ilarity 75.9%; Pred. No. 2.1e-41;
Conservative 15; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single chain Fv protein sequence shPM1(deltaEL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 7; Page 80-82; 120pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                         AAY55075 standard; Protein; 260 AA.
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|DYWGQGSLVTVSS 138
                                                                                                                                                                                                                            DYWGQGTSVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                   25-FEB-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tsuchiya M, Saito M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-039382/03.
                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAZ40305
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Query Match
Best Local Simil
Matches 101; C
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                                                                                                                                                                                                                                                                                                   Human, antibody, interleukin-6; receptor; IL-6R; CDR; PCR;
complemantarity determining region; mouse; monoclonal; hybridoma;
plasmid; polymerase chain reaction; amplify.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 has low antigenicity and contains mouse V-region complementarity determining regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reconstituted human antibody to human interleukin-6 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tsuchiya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saldanha JW, Sato K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 142-3; 207pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "Leader peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                              AAR29014 standard; Protein; 138 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56..69
/label= FR2
70..85
/label= CDR2
86..117
/label= FR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118.:127
/label= CDR3
128.:138
/label= FR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50..55
/label= CDR1
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/label= FR1
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92JP-0032084
 137
                     126 DYWGQGSLVTVSS 138
                                                                                                                                                                                                       (updated)
(first entry)
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DYWGQGTSVTVSS
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19-FEB-1992;
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30-MAR-1993
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Region

Region

Sequence

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75.98;

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Best Local Similarity
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                                                                                                             66 EWIGYISYSGITTYNPSLKSRVTMLRDTSKNQFSLRLSSVTAADTAVYYCARSLARTTAM 125
                                                                                               65 EWMGYISYSGITTYNPSLKSRISITRDISKNOFFLOLNSVTTGDISTYYCARSLARTTAM 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a single chain FV (ScFV) sequence.

The invention relates to a method for isolating a gene encoding a membrane-bound protein, comprising introducing a vector into a cell, contacting an antigen with the cell expressing the fused protein encoded by the vector on its surface to select an antigen-binding cell, and isolating the cDNA. The vector contains DNA encoding a secretable functional protein with antigenicity and binding affinity, and a CDNA ligated to DNA downstream of the 3' end of the coding sequence. The method can be used to isolate a membrane-bound protein for diagnosis and study. It can also be used for producing drugs treating abnormal functions of the protein. Such a technique is efficient and selective, which is different from the prior-art transmembrane trap (TMT) method wherein an epitope recognised by an antibody is carried in a fused
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                                                                                                                                                                                                                                                                                                                            Gene isolation; membrane-bound protein; fusion protein; drug production; antigen-binding cell; secretable functional protein; antigenic protein; protein isolation; diagnosis; ScFv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Efficient and selective isolation of a gene encoding membrane protein with low or no antigenic binding activity, for diagnosis, study of, and production of drugs treating abnormal functions of the protein -
                                                              6 ILFLVATATGVDSQVQLQESGFGLVRPSQTLSLTCTVSGYSITSDHAMSWVRQPPGRGL
                                                 5 ILLWLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKL
                          Gaps
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 Length 260;
                         Indels
                           17;
 DB 21;
  537; DB 21
No. 5.3e-41
                                                                                                                                                                                                                                                                                                          Single chain Fv protein sequence shPM1-Kappa.
  74.8%; Score 537; DB 75.9%; Pred. No. 5.3e-ive 15; Mismatches
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                                                                                                                                                                                                                                  AAY55078 standard; Protein; 367 AA.
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                                                                                                                                               125 DYWGOGTSVTVSS 137
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126 DYWGQGSLVTVSS 138
                                                                                                                                                                                                                                                                                  (first entry)
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Query Match
Best Local Similarity 75.9
Matches 101; Conservative
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N-PSDB; AAZ40308.
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AAY55078
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74.8%; Score 537; DB 21; Length 367;

Query Match

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                                                                                                                                                                                             EWMCYISYSGITTYNPSLKSRISITRDTSKNOFFLOLNSVTTGDTSTYYCARSLARTTAM 124
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The invention relates to a method for isolating a gene encoding a membrane-bound protein, comprising introducing a vector into a cell, contacting an antigen with the cell expressing the fused protein encoded by the vector on its surface to select an antigen-binding cell, and isolating the CDNA. The vector contains DNA encoding a secretable functional protein with antigenicity and binding affinity, and a CDNA ligated to DNA downstream of the 3' end of the coding sequence. The method can be used to isolate a membrane-bound protein for diagnosis and study. It can also be used for producing drugs treating abnormal functions of the protein. Such a technique is efficient and selective, which is different from the prior-art transmembrane trap (TWT) method wherein an epitope recognised by an antibody is carried in a fused
                                                                                    64
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                                                                                                                 5 ILLWLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKL
                             Gaps
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                             Indels
7.8e-41;
ches 17;
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Pred. No. 8.1e-41;
  Pred. No. 7.8e-
5; Mismatches
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                             15;
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75.9%;
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98JP-0279876.
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DYWGQGSLVTVSS 138
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                             Matches 101; Conservative
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N-PSDB; AAZ40309.
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Best Local Similarity
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01-OCT-1998;
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1LLWLFTAFPG11LSDVQLQESGPVLVKPSQSLSLTCTVTGYS1TSDHAWSW1RQFPGNKL
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                                                                                                                                                         This sequence represents a single chain Fy (ScFv) sequence. The invention relates to a method for isolating a gene encoding a membrane-bound protein, comprising introducing a vector into a cell, contacting an antigen with the cell expressing the fused protein encoded by the vector on its surface to select an antigen-binding cell, and isolating the cDNA. The vector contains DNA encoding a secretable functional protein with antigenicity and binding affinity, and a CDNA ligated to DNA downstream of the 3' end of the coding sequence. The method can be used to isolate a membrane-bound protein for diagnosis and study. It can also be used for producing drugs treating abnormal functions of the protein. Such a technique is efficient and selective,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene isolation; membrane-bound protein; fusion protein; drug production; antigen-binding cell; secretable functional protein; antigenic protein; protein isolation; diagnosis; ScFv.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      functions of the protein. Such a technique is efficient and selective, which is different from the prior-art transmembrane trap (TMT) method wherein an epitope recognised by an antibody is carried in a fused
                                            ILLWLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKL
                                                                EWMGYISYSGITTYNPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLARTTAM
  0; Gaps
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  17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Single chain Fv protein sequence shPM1(deltaEL)-BvGS3.
  15; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                AAY55080 standard; Protein; 519 AA.
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98JP-0279876.
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Best Local Similarity 75.9
Matches 101; Conservative
101; Conservative
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N-PSDB; AAZ40312.
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01-OCT-1998;
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                                                                                                         66 EWIGYISYSGITTYNPSLKSRVTMLRDTSKNQFSLRLSSVTAADTAVYYCARSLARTTAM 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a single chain Fv (SCFV) sequence.

The invention relates to a method for isolating a gene encoding a membrane-bound protein, comprising introducing a vector into a cell, contacting an antigen with the cell expressing the fused protein encoded by the vector on its surface to select an antigen-binding cell, and isolating the CDNA. The vector contains DNA encoding a secretable functional protein with antigenity and binding affinity, and a CDNA ligated to DNA downstream of the 3' end of the coding sequence. The method can be used to isolate a membrane-bound protein for diagnosis and study. It can also be used for producing drugs treating abnormal functions of the protein. Such a technique is efficient and selective, which is different from the prior-art transmembrane trap (TMT) method wherein an epitope recognised by an antibody is carried in a fused
65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene isolation; membrane-bound protein; fusion protein; drug production; antigen-binding cell; secretable functional protein; antigenic protein; protein isolation; diagnosis; SCFv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Efficient and selective isolation of a gene encoding membrane protein with low or no antigenic binding activity, for diagnosis, study of, and production of drugs treating abnormal functions of the protein
6 IILFLVATATGVDSQVQLQESGPGLVRPSQTLSLTCTVSGYSITSDHAWSWVRQPPGRGL
                                                                     EWMGYISYSGITTYNPSLKSRISITRDTSKNOFFLOLNSVTTGDTSTYYCARSLARTTAM
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75.9%; Pred. No. 1.2e-40;
live 15; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single chain Fv protein sequence hPM1-BvGS3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY55074 standard; Protein; 546 AA.
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                                                                                                                                                                                                            125 DYWGOGTSVTVSS 137
                                                                                                                                                                                                                                                                                 DYWGOGSLVTVSS 138
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Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tsuchiya M, Saito M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-039382/03.
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The invention relates to a method for isolating a gene encoding a membrane-bound protein, comprising introducing a vector into a cell, contacting an antigen with the cell expressing the fused protein encoded by the vector on its surface to select an antigen-binding cell, and isolating the cDNA. The vector contains DNA encoding a secretable functional protein with antigenicity and binding affinity, and a cDNA ligated to DNA downstream of the 3' end of the coding sequence. The method can be used to isolate a membrane-bound protein for diagnosis and study. It can also be used for producing drugs treating abnormal functions of the protein. Such a technique is efficient and selective, the coding sequence of the coding sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Efficient and selective isolation of a gene encoding membrane protein with low or no antigenic binding activity, for diagnosis, study of, and production of drugs treating abnormal functions of the protein
               6 IILFLVATATGVDSQVQLQESGPGLVRPSQTLSLTCTVSGYSITSDHAWSWVRQPPGRGL
   ILLWLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKL
                                                 EWMGYISYSGITTYNPSLKSRISITRDTSKNOFFLQLNSVTTGDTSTYYCARSLARTTAM
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wherein an epitope recognised by an antibody is carried in a fused
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.8%; Score 537; DB 21; Length 626; 75.9%; Pred. No. 1.4e-40;
                                                                                                                                                                                                                                                 Single chain Fv protein sequence shPM1-kappa-BvGS3.
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                                                                                                                                                                            AAY55081 standard; Protein; 626
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98JP-0279876
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126 DYWGQGSLVTVSS 138
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                                                                                                                                                                                                                          (first entry)
                                                                                              125 DYWGOGTSVTVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saito M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000-039382/03.
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N-PSDB; AAZ40316.
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                                                                                                                                                                                                                                                                                                                    Synthetic.
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124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene isolation; membrane-bound protein; fusion protein; drug production; antigen-binding cell; secretable functional protein; antigenic protein; protein isolation; diagnosis; SCFv.
EWMGYISYSGITTYNPSLKSRISITRDISKNOFFLOLNSVTTGDTSTYYCARSLARTTAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Efficient and selective isolation of a gene encoding membrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      with low or no antigenic binding activity, for diagnosis, study production of drugs treating abnormal functions of the protein
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ilarity 75.9%; Pred. No. 1.4e-40;
Conservative 15; Mismatches 17;
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                                                                                                                                                                     126 DYWGOGSLVTVSS 138
                                                                                                                              125 DYWGQGTSVTVSS 137
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01-OCT-1998;
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Matches 101;
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Gaps

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17; Indels

15; Mismatches

Matches 101, Conservative

Best Local Similarity

5 ILLWLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKL 64

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Search co
                            Db
   8
                                                   66 EWIGYISYSGITTYNPSLKSRVTWLRDTSKNQFSLRLSSVTAADTAVYYCARSLARTTAM 125
                                 EWMGYISYSGITTYNPSLKSRISITRDISKNQFFLQLNSVTTGDISTYYCARSLARTTAM 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGNKLEWMGYISYSGSTSY 60
6 IILFLVATATGVDSQVQLQESGPGLVRPSQTLSLTCTVSGYSITSDHAWSWVRQPPGRGL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 DVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMGYISYSGITTY 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents the heavy chain variable region for monoclonal antibody (MAD) 13D10, which immunoreacts with a lead cation. The sequence was derived from RNA isolated from mouse hybridom cells. The protein can be used for binding heavy metals, such as lead cations. It can be used for detecting, removing, adding or neutralising the heavy metals in biological and inanimate systems. It can be used in e.g. aqueous liquid systems, in biological or environmental systems or in such compositions as perfumes, cosmetics, pharmaceuticals, health care products, skin treatment products, pesticides, herbicides, solvents used in the production of semi-conductor and integrated circuit components and production materials for electronic components. The products can provide for applications involving minute amounts of
                                                                                                                                                                                                                                                                                                                                                      Monoclonal antibody, Fd fragment, lead cation, perfume, cosmetic, pharmaceutical, health care, skin treatment, pesticide, herbicide, heavy metal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding heavy metal binding polypeptide sequences - used for detecting, removing, adding or neutralising heavy metals, such as lead cations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74.4%; Score 534; DB 18; Length 119; 85.7%; Pred. No. 4.1e-41; ive 6; Mismatches 11; Indels (
                                                                                                                                                                                                                                                                                                                       Lead binding MAb 13D10 heavy chain variable region.
                                                                                                                                                                                                                       AAW01584 standard; Protein; 119 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lopez O, Murray PJ, Wylie DE;
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Best Local Similarity 85.7
Matches 102; Conservative
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N-PSDB; AAT58258.
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05-JUN-1995;
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1 MRVLILLWLFTAFPGILSDV.......LARTTAMDYWGQGTSVTVSS
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(c) 1993 - 2003 Compugen Ltd.
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HVMS1B
AVMS35
C53285
I28195
S38718
S07637
T01262
HVMS31:
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G2MS60
D25114
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seq length: 200000000
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Match Length DB
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106
120
         Copyright
                                                           October 22,
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Ig heavy chain - h	Ig heavy chain - h	Ig heavy chain V r	Ig mu heavy chain	Ig heavy chain pre	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain pre	Ig heavy chain.pre	Ig mu heavy chain	Y V rieds wread ST					
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R;Near, R.I.; Haber, E.
Mol. Immunol. 26, 371-382, 1989
A;Title: Characterization of the heavy and light chain immunoglobulin variable region ge.
A;Reference number: PL0100; MUID:89238344; PMID:2497340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M27660; NID:g341745; PIDN:AAAS8746.1; PID:g609530
A;Experimental source: strain A/J
A;Note: the VH40-140 gene segment is classified as a member of the 36-60 VH gene family C;Genetics:
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C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 23-Jul-1999
C;Accession: S3075
S;Grant, F.J.; Levin, S.D.; Gilbert, T.; Kindsvogel, W.
Nucleic Acids Res. 15, 5496, 1987
A;Title: Improved RNA sequencing method to determine immunoglobulin mRNA sequence.
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                                                                                                                                               Ig heavy chain precursor V region (40-140) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MRVLILLWLFTAFPGGLSDVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWSWIRQFP
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 84.1%; Score 603.5; DB 2; Best Local Similarity 84.7%; Pred. No. 9.9e-46; Matches 116; Conservative 8; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.Keywords: heterotetramer; immunoglobulin
F;1-18/Domain: signal sequence #status predicted <81
F;19-115/Domain: V segment #status predicted <VRE>
F;33-116/Domain: immunoglobulin homology <IMM>
F;117-118/Domain: D segment #status predicted <DRE>
F;117-118/Domain: J segment #status predicted <DRE>
ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-135 <NEA>
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A; Molecule type: DNA
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A; Reference number: JT0501; MUID:89279149; PMID:2499654
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Best Local Similarity 90.5%;
Matches 105; Conservative
                    A; Accession: JT0508
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R;Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
J. Exp. Med. 169, 2007-2019, 1989
A;Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ly heavy Custin precules (Nov-1988 #text_change 18-Oct-1996 C; Species; Mus musculus (house mouse)
C; Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 18-Oct-1996 C; Accession: B24672
R; Winter, E.; Radbruch, A.; Krawinkel, U.
EMBO J. 4, 2861-2867, 1985
A; Reference number: A91022; MUID:86055722; PMID:2998759
A; Reference number: A91022; MUID:86055722; PMID:2998759
A; Residues: 1.134 < WIN>
A; Residues: 1.134 < WIN>
A; Residues: 1.134 < WIN>
A; Residues: 15/1
C; Genetics:
A; Introns: 15/1
C; Superfanily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin nomology
C; Keywords: heterotetramer; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin homology c; Keywords: immunoglobulin homology c; Keywords: immunoglobulin homology < IMM>
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Species: Mus musculus (house mouse)
Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 18-Oct-1996
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C;Species: Wus musculus (house mouse)
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 16-Aug-1996
C;Accession: JT0508
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Reference number: S30751; MUID:87260030; PMID:3601683
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Pred. No. 9.1e-45;
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82.5%;
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Best Local Similarity 84.7%;
Matches 116; Conservative
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Best Local Similarity
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A;Molecule type: DNA
A;Residues 1.15./G',16-137 <RI2>
A;Residues 1.15./G',16-137 <RI2>
A;Cross.references: EMBL:X07880; NID:g51760; PIDN:CAA30727.1; PID:g295908
A;Jilka, R.L.; Pestka, S.
B;Jilka, R.L.; Pestka, S.
Broc. Natl. Acad. Soi. U.S.A. 74, 5692-5696, 1977
A;Title: Amino acid sequence of the precursor region of MOPC-315 mouse immunoglobulin he A;Reference number: A93814; MUID:78094475; PMID:414225
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A;Residues: 19-52, R',53-75, BYGB', 80-101,'D',103-106,'ZB',109-122,124-137 <FRA>
R;Hood, L.; Margolles, M.; Givol, D.; Zakut, R.
unpublished results, cited by Padlan, E.A., Davies, D.R., Pecht, I., Givol, D., and Wrig
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A,Molecule type: protein
A,Rolecule type: protein
A,Residues: 1-14, "16-31 <JIL>
A,Residues: 1-14, "16-31 <JIL>
A,Residues: 1-14, "16-31 <JIL>
A,Residues: 1-14, "16-31 <JIL>
A,Rote: the authors translated mRNA in vitro to obtain the precursor protein
R,Schechter, I: Wolf, O.; Zemell, R.; Burstein, Y.
Fed. Proc. 38, 1839-1845, 1979
A,Title: Structure and function of immunoglobulin genes and precursors
A,Reference number: A91462; MUID: 79148758; PMID: 428562
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A;Residues: 1, 'X', 3-11, 'X', 14-21 <SCH>
A;Note: the authors translated mMA in vitro to obtain the precursor protein
R;Francis, S.H.; Leslie, R.G.O.; Hood, L.; Eisen, H.N.
Proc. Natl. Acad. Sci. U.S.A. 71, 1123-1127, 1974
A;Title: Amino-acid sequence of the variable region of the heavy (alpha) chai
A;Reference number: A93787; MUID:74170779; PMID:4524622
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A)Status: translation not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-116 <LEV>
A;Experimental source: strain BALB/cJ
A;Note: this sequence belongs to the VH3660 subfamily
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin sequence #status predicted <SIG>F;1-18/Domain: signal sequence #status predicted <SIG>F;19-116/Product: Ig heavy chain V region (LB43) #status predicted <MAT>F;33-116/Domain: immunoglobulin homology <IMM>
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A;Residues: 1-137 <RIN>
A;Cross-references: GB:M27638; NID:g602706; PIDN:AAA61337.1; PID:g602707
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Pred. No. 1.6e-40;
4; Mismatches 7; Indels
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submitted to the EMBL Data Library, June 1988
A;Reference number: S03262
A;Accession: S03262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Experimental source: strain MOPC
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A;Accession: 128195
A;Molecule type: mRNA
A;Residues: 1-17 < SHE)
A;Cross-references: GB:M19775; NID:g195526; PIDN:AAA38343.1; PID:g195527
A;Note: the authors translated the codon AAC for residue 61 as Thr, and did not translate c;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin v region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig heavy chain V region (PTF.02) - mouse (Species: Mus musculus (house mouse) (5) pecies: Mus musculus (house mouse) (5) pecies: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 23-Jul-1999 (5) Accession: 807637 (5) Accession: 807637 (7) Pelyyanovsky, 0.L. (7) R; Urakov, D.N.; Deev, S.M.; Polyanovsky, 0.L. (7) Muscleic Acids Res 17, 9481, 1989 (7) Affile: The structure of the expressible VH gene from a hybridoma producing monoclonal A; Reference number: 807637; MUID:90067954; PMID:2587273
                                                                                                                                     Hypervariable region amino
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: S3718
R;Cimanis, A.Y.
Submitted to the EMBL Data Library, November 1993
A;Reference number: S38713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X76018; NID:9416102; PIDN:CAA53605.1; PID:91334263
                          01-Dec-1989 #sequence_revision 30-Sep-1991 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DVQLQESGPGLVKPSQSLSLTCAVTGYSITSDYAWNWIRQFPGNKLEWMGYISYSGTTNY
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C;Keywords: heterotetramer; immunoglobulin
F;I5-98/Domain: immunoglobulin homology <IMM>
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                                                                              R.Sherman, M.A.; Deans, R.J.; Bolger, M.B.
J. Blod. Chem. 263, 4059-4063, 1988
A;Title: Haloperidol binding to monoclonal antibodies. B
A;Reference number: A28195; MUID:88153717; PMID:3267217
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 532; DB 2; L
Pred. No. 1.4e-39;
6; Mismatches 9;
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Pred. No. 1.4e-38;
5; Mismatches 11;
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C;Species: Mus musculus (house mouse)
C;Date: 01-Dec-1989 #sequence_revisio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 84.0%;
Matches 100; Conservative
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al Similarity 85.7%;
102; Conservative
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A,Molecule type: DNA
A,Residues: 1-136 <URA>
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A;Molecule type: mRNA
A;Residues: 1-116 <CIM>
                                                          C;Accession: I28195
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              A; Contents: annotation; revision to residue 53
R; Cheadle, C.; Hook, L.E.; Givol, D.; Ricca, G.A.
R) Cheadle, C.; Hook, L.E.; Givol, D.; Ricca, G.A.
R) Lannoll. 129, 21-30, 1992
A; Title: Cloning and expression of the variable regions of mouse myeloma protein MOPC315
A; Reference number: 823599; MUID:92114886; PMID:1731188
A; Recession: 823599
A; Molecule type: mRNA
A; Residues: 19-137 cKHE
A; Residues: 19-137 cKHE
A; Cross-references: EMBL:X63972; NID:953532; PIDN:CAA45384.1; PID:9938267
C; Comment: This alpha chain was isolated from a myeloma protein that has anti-dinitrophe A; Introns: 15/1
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Ig heavy chain V and J regions, monoclonal antibody OHP7D7.2.3 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C;Accession: C53285
R;Sawada, J.; Mizusawa, S.; Terao, T.; Naito, M.; Kurosawa, Y.
Mol. Immunol. 28, 1063-1072, 1991
A;Title: Molecular characterization of monoclonal anti-steroid antibodies: primary struct and their pH-reactivity profiles.
A;Reference number: A53285; MUID:92017897; PMID:1922102
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KGWwords: heterotetramer; immunoglobulin
F;1-18/Domain: signal sequence #status experimental <SIG>
F;19-136/Product: Ig heavy chain V region (MOPC 315) #status experimental
F;33-116/Domain: immunoglobulin homology <IMM>
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A;Cross-references: GB:D12734; NID:g220548; PIDN:BAA02226.1; PID:g220549
A;Cross-references: GB:D12734; NID:g220548; PIDN:BAA02226.1; PID:g220549
A;Note: sequence extracted from NOSI backbone (NCBIN:63297, NCBIP:63302)
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 538; DB 1;
; Pred. No. 5.1e-40;
15; Mismatches 21;
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84.9%; Pred. No. 6.6e-40;
ive 6; Mismatches 12;
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Best Local Similarity 73.7%
Matches 101, Conservative
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A;Molecule type: mRNA; protein
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  A;Reference number: A94484
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Best Local S
Matches 101
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C;Species: Mus musculus (house mouse) .
C;Daccession: 837200
R;Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.
submitted to the EMBL Data Library, August 1993
A;Description: Production and cloning of TMV-specific monoclonal antibodies.
                                                                                                                                                                                      1 MKVLSLLYLLTAIPGILSDVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYYWNWIRQFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITSSYYWNWIRQFPGNKLEWMGYISYDGRNDY
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                                                                                                                                                             1 MRVLILLWLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFP
                                                                                                                                                                                                                                             GNKLEWMGYISYSGITTYNPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCAR 116
                                                                                                                                                                                                                                                                  DVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMGYISYSGITTY
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                     predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 121;
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                       11; Indels
                                                                                  Length
  <SIG>
#status |
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1.5e-35;
ches 17;
                                                                               Score 510; DB 1;
Pred. No. 1.2e-37;
8; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 479; DB 2;
Pred. No. 6.1e-35;
5; Mismatches 14,
F;1-18/Domain: signal sequence #status predicted F;19-116/Product: Ig heavy chain V region (M315) F;33-116/Domain: immunoglobulin homology <IMM>
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Pred. No. 1.5e-
8; Mismatches
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8
                                                                                  71.0%;
83.6%;
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Best Local Similarity 77.7%;
Matches 94; Conservative
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78.2%;
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Best Local Similarity 78.2
Matches 93, Conservative
                                                                                                                         Conservative
                                                                                                    Similarity
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-121 <FIS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-119 <OLL>
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Best Local
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Matches
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  PIDN:CAA34714.1; PID:g297543
for residue 112 as Ile, TAC for residue
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                                                                                                                                                                                                                                                                                                                                                      61 GNKLEWMGYISYDGSNGYNPSLKNRISITRDTSKNQFFLKLNSVTTEDTATYYCTRG--- 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79 NPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLARTTAMDYWGQGTSVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C,Accesion: T01267
R,Pirofski, L.A.; Thomas, E.K.; Scharff, M.D.
AIDS Res. Hum. Retrovitues 9, 41.49, 1993
A;Title: Variable region gene utilization and mutation in a group of neutral A;Reference number: Z14285; MUID:99152285; PMID:7678971
A,Accession: T01262
A,Accession: T01264
A,Residues: preliminary; translated from GB/EMBL/DDBJ
A,Residues: 1-114 <PIR>A,Residues: 1-114 <PIR>A,Residues: 1-114 <PIR>B,Residues: Inmunoglobulin V region; immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g heavy chain precursor V region (M315) - mouse
;Species: Mus musculus (house mouse)
jbate: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 16-Aug-1996
;Accession: JT0509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species: Mus musculus (house mouse)
| Species: Mus musculus (house mouse)
| Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                    1 DVQLQQSGPGLVKPSQSLSHTCTVTGYSITSDYAWNWIRQFPGNKLEWMGYISFSGSTSY
                                                                                                                                                                                                                                               1 MRVLILLWLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 DVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMGYISYSGITTY
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د.
                                                                                                                                                             Length 136;
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                                                                                  immunoglobulin homology
                                                                                                                                                                                                       Indels
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                                                                                                                                                             Score 519.5; DB 2;
Pred. No. 2.1e-38;
9; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 517.5; DB 2;
Pred. No. 2.6e-38;
8; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                          A;Introns: 15/3
C;Superfamily: immunoglobulin V region; immunog
C;Keywords: heterotetramer; immunoglobulin
F;33-116/Domain: immunoglobulin homology <IMM>
  Cross-references: EMBL:X16740; NID:952099; Note: the authors translated the codon TAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    heavy chain V region - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                    ----DGYHFFTYWGQGTLVTVSA 136
                                                                                                                                                                                                                                                                                                                                                                                                           121 TTAMD-----YWGQGTSVTVSS 137
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72.1%;
Best Local Similarity 83.2%;
Matches 99; Conservative
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Best Local Similarity 72.7%;
Matches 104; Conservative
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                                          Genetics:
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RESULT 11

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136

78 9

Gaps

5;

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Gaps

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RESULT 15
D33932
Ig mu chain precursor V region (E7) - mouse
C;Species: Wus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 23-May-1997
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 23-May-1997
C;Accession: D33932
R;Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.
R;Reference number: A33932; MUD:89282823; PMID:2499887
A;Reference number: A33932; MUD:89282823; PMID:2499887
A;Accession: D33932
A;Status: preliminary
A;Molecule type: mRNA
A;References: GB:M21106
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;33-115/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                              KESULI 13

S26464

Ig heavy chain V region - mouse

Ig heavy chain V region - mouse

C; Speciess Mus musculus (house mouse)

C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C; Accession: S26464

R; Kavaler, J.

R; Ravaler to the EMBL Data Library, April 1991

A; Reference number: S26459

A; Accession: S26664

A; Residues preliminary

A; Molecule type: mRNA

A; Residues: 1-106 < KAVA

A; Residues: 1-106 < KAVA

A; Cross-references: EMBL: K59114; NID: G51926; PIDN: CAA41840.1; PID: G51927

C; Superfamily: immunoglobulin V region; immunoglobulin homology

C; Keywords: heterotetramer; immunoglobulin

F; 3-86/ Domain: immunoglobulin homology < IMM>
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  78
                            1 DVQLQESGPGLVKPSQSLSLTCSVTGXSITSGYYWNWIRQFPGNKLEWMGYISYDGSHNY 60
                                                                                                           79 NPSLKSRISITRDISKNOFFLQLNSVITGDISTYYCARSL-----ARTTAMDYWGQGT 131
                                                                                                                                        61 NPSLKARISITRDTSKNQFFLKLNSVTIEDTATYYCARPLYYRYDEEYYYAMDYWGQGT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 KPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMGYISYSGITTYNPSLKSRISITR 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KPSQSLSLTCTVTGYSTTSDYAWNWIRQFPGNKLEWMGYISYSGSTSYNPSLKSRISITR 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.6%; Score 478.5; DB 2; Length 106; 84.1%; Pred. No. 5.9e-35; ive 8; Mismatches 8; Indels 1;
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Best Local Similarity 81.0%; Pred. No. 7.9e-35;
Matches 94; Conservative 11; Mismatches 10; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 66.6%;
Best Local Similarity 84.1%;
Matches 90; Conservative
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Search completed: October 22, 2003, 22:18:06 Job time : 26.947 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

October 22, 2003, 22:10:20 ; Search time 14.0114 Seconds (without alignments) 459.817 Million cell updates/sec

Title: US-09-114-285A-31
Perfect score: 718
Sequence: 1 MRVLILLWLF7AFPGILSDV......LARTTAMDYWGQGTSVTVSS 137

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

127863 Total number of hits satisfying chosen parameters: 127863 segs, 47026705 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P18532 mus musculu	32	P18531 mus musculu	P18533 mus musculu	. P01823 mus musculu	319 mus n	P06331 homo sapien	xenor		mus m		homod	mus m		homo	homo	homo	homo	พนธ แ	P01751 mus musculu	P01746 mus musculu	mus m	homo) homo	4 homo	homo	homo	แนธ ก	mus	P01759 mus musculu	mus	181	P01771 homo sapien
SUMMARIES	ID	HV61 MOUSE	HV46 MOUSE	HV60 MOUSE	HV62 MOUSE	HV47 MOUSE	HV43_MOUSE	HV2I HUMAN	HV02_XENLA	HV2G_HUMAN	HV44 MOUSE	HV2F HUMAN	HV2E_HUMAN	HV45 MOUSE	HV01_XENLA	HV2C_HUMAN		HV2D_HUMAN		HV16 MOUSE	HV07_MOUSE	HV02_MOUSE	HV11_MOUSE	HV3F_HUMAN	HV3H_HUMAN	HV2A_HUMAN	HV3L_HUMAN	HV3G HUMAN				HV03_MOUSE	HV42_MOUSE	HV3J_HUMAN
	DB	_ -	-	-4	-	-	Н	П	-	Н	Н	~	Н	Н	ч	-	Н	~	-	ч	Н	Н	~	Н	Н	Н	Н	Н		Н	-	н	Н	Н
	Length	116	137	116	117	113	144	146	135	117	115	129	121	116	136	119	147	125	120	136	139	140	3	115	3	2	119	N	117	$\overline{}$	136	120	117	
* C	Match	75.6	74.9	71.0	64.3	ς.	53.6	52.6	47.1	ģ	46.0	٠	45.0			42.9	ä	ä	ö		٥.	40.0	σ.	o,	ъ.	ъ В	œ	а Э	8	æ	œ	ω.	7.	
	Score	543	538	510	461.5		384.5		338	337	330	328	323	316	312.5		295.5	295	291.5	289.5	287.5	287	285.5			277.5	N	276.5	276	274	274	273	7	272
7	No.		7	е	4	ហ	9	7	8	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

P01805 rattus norv P01756 mus musculu	P01762 homo sapien P01772 homo sapien	P01810 mus musculu	POILS mus musculu	PO6330 mus musculu	P01808 mus musculu	P01764 homo sapien	P01811 mus musculu	P18525 mus musculu
HV01_RAT HV12_MOUSE	HV3A_HUMAN HV3K_HUMAN	HV40_MOUSE	HV14 MOUSE	HVS1_MOUSE	HV38_MOUSE	HV3C HUMAN	HV41 MOUSE	HV54_MOUSE
		п.	٦,	- - -	-	ч	႕	П
142	122 126	119	117	118	119	117	117	117
37.9	37.1	37.0	9.0	36.8	36.8	36.5	36.5	36.5
272 271	266.5	265.5	265	264.5	264.5	262	262	262
9.8 4.73	36	38	o	4 4 0 L	42	43	44	45

ALIGNMENTS

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RESULT 2

FRAMEWORK-3

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                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-21.
MEDLINE=79148758; PubMed=428562;
Schechter I., Wolf O., Zemell R., Burstein Y.;
"Structure and function of immunoglobulin genes and precursors.";
Fed. Proc. 38:1839-1845(1979).
                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=74170779; PubMed=4524622; Francis S.H., Leslie R.G.Q., Hood L., Eisen H.N.; Manno-acid sequence of the variable region of the heavy (alpha) chain of a mouse myeloma protein with anti-hapten activity."; Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=17244979; Pubmed=268248; Hood L., Margolies M.N., Givol D., Zakut R.; Unpublished results, cited by: Unpublished results cited by: Padlan E.A., Davies D.R., Peter I., Givol D., Wright C.; Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).
-!- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT HAS ANTI-DINITROPHENYL ACTIVITY.
                                                                                                                                                     MEDLINE-89238351; PubMed-2497341;
Rinfret A., Horne C., Dorrington K.J., Klein M.;
"Cloning, sequencing and expression of the rearranged MOPC 315
                                                                                                                                                                                                                        SEQUENCE OF 1-31.
MEDLINE=78094475; PubMed=414225;
Jilka R.L., Pestka S.;
"Amino acid sequence of the precursor region of MOPC-315 mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IG HEAVY CHAIN V REGION MOPC 315.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696 (1977).
                                   21-JUL-1986 (Rel. 01, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
             137 AA
                                                                      Ig heavy chain V region MOPC 315 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HASP, PO1825, 7FAB.

HICEPPEO, IPRO07110; Ig-like.

INTERPEO, IPRO3306; Ig_W.

Ffam, PP0047; ig; 1.

SMART, SMO046; IGV; 1.

RPOSITE; PS50835; IG_LIKE; 1.

M Immunoglobulin V region; Signal.

T SIGNAL

19 137 FRAME
FRAME
                                                                                                                                                                                                  dol. Immunol. 26:431-434 (1989)
                                                                                                                                                                                                                                                                   immunoglobulin heavy chain."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M27638; AAA61337.1; -. EMBL; X07880; CAA30727.1; -.
              STANDARD;
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54
68
84
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                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 19-136.
                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                 NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              REVISION TO 53
                                                                                                                                                                                        gene segment.
             MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GNKLEWLGFIKYDGSNGYNPSLKNRVSITRDTSENQFFLKLNSVTTEDTATYYCAGDNDH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MRVLILLWLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFP
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BALDINE=82929494;

BEDLINE=8252949;

Levy N.S. Malipiero U.V., Lebecque S.G., Gearhart P.J.;

Levy N.S. Malipiero U.V., Lebecque S.G., Gearhart P.J.;

"Early onset of somatic mutation in immunoglobulin VH genes during

"Early onset of somatic mutation in immunoglobulin VH genes during

"Early onset of somatic mutation in immunoglobulin VH genes during

"Early onset of somatic mutation in immunoglobulin VH genes during

"Early onset of somatic mutation in immunoglobulin VH genes during

"Early No." | The primary immunor response.";

"The primary immunor response.";
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
G -> GG (IN REF. 1; CAA30727).
G -> H (IN REF. 2).
G -> H (IN REF. 4).
N -> D (IN REF. 4).
MISSING (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                       74.9%; Score 538; DB 1; Length 137; 73.7%; Pred. No. 2.6e-45; ive 15; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 510; DB 1; Length 116;
Pred. No. 1.1e-42;
8; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IG HEAVY CHAIN V REGION M315.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2
                                                                                                                                                                                                                                                                                                                      15399 MW; FB3828304C2B81DC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V region M315 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596, Ig_MC.
Pfam; PF00047; ig; 1.
SMART; SM00406, IGV; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 LYYFDYWGQGTTLTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 TTAMDYWGQGTSVTVSS 137
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83.6%;
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                                                                                                                                                                                                                                                                                                                         137 AA;
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STRAIN=A/J;
MEDLINE=84024551; PubMed=6414509;
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P01819;
                                                                                            idiotype.
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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1 MRVLILLWLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITS-DHAWSWIRQF 59
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TEATLY onset of sometic mutation in immunoglobulin VH genes during
The primary immune response.";
J. Exp. Mad. 169:2007-2019(1989).
-!- SMILANITY: Contains 1 immunoglobulin-like domain.
PIR; JT0510; HVMS73.
R PIR; JT0510; HVMS73.
R InterPro; IPR003106; Ig_MHC.
R InterPro; IPR003596; Ig_MHC.
R InterPro; IPR003596; Ig_WHC.
R SMART; SM00406; IGv; 1.
R SMART; SM00406; IGv; 1.
R PROSITE; PS50835; IG_LIKE; 1.
R Immunoglobulin V region; Signal.
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                                                                                              61 GNKLEWMGYISYDGSNNYNPSLKNRISITRDTSKNQFFLKLNSVTTEDTATYYCAR 116
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                            GNKLEWMGYISYSGITTYNPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IG HEAVY CHAIN V REGION 733.
IG-LIKE.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 117
117 AA; 13223 MW; 1595517827F976BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P01823;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
16-Bray chain V region 36-60.
                                                                                                                                                                                                                                           01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                                                      Ig heavy chain V region 733 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=BALB/CJ;
MEDLINE=89279149; PubMed=2499654;
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Best Local Similarity 74.4
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                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117
>117
115
115
                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                      HV62 MOUSE
P18533;
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN ANTIARSONATE MONOCLONAL ANTIBODY OF THE IGG2A SUBCLASS. IT REPRESENTS A SECOND IDTOTYPE FAMILY CHARACTERISTIC OF THE ANTIARSONATE RESPONSE OF STRAIN A/J MICE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 DVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMGYISYSGITTY
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MEDLINE=81012133; PubMed=6774258;
Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
"Two types of somatic recombination are necessary for the generation of complete immunoglobulin heavy-chain genes.";
Nature 286:676-683(1980).
Juszczak E.C., Margolies M.N.; "Amino acid sequence of the heavy chain variable region from the A/J mouse anti-arsonate monoclonal antibody 36-60 bearing a minor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -:- MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A DIFFERENTIATED GENE ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 62.7%; Score 450; DB 1; Length 11 Best Local Similarity 74.8%; Pred. No. 6.8e-37; Matches 89; Conservative 12; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 AA; 12734 MW; 38DC0E0E3F5075B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
25-SEP-2003 (Rel. 42, Last annotation update)
15 heavy chain V region MOPC 141 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfan; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; 3D-structure.
NON TER 113 113
                                                                                                                                         Biochemistry 22:4291-4296(1983)
                                                                                                                                                                                                                                                                                                    PIR, A02098, G2MS60.
PDB, 1J10, 18-FEB-03.
PDB, 1J17, 18-FEB-03.
PDB, 1J1X, 18-FEB-03.
InterPro, IPR00710, Ig-like.
InterPro, IPR003006, Ig_MHC.
InterPro, IPR003596, Ig_W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
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                                                                                                                                                  66 EWIGEINHSGSTNYKTSLKSRVTISLDTSKNLFSLKLSSVTAADTAVYYCARGLLRGGWN 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 LEWMGYISYSGITTYNPSLKSRISITRDTSKNOFFLQLNSVTTGDTSTYYCARSLARTTA 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=88176921; PubMed=2451244; Schiner L.A.; Schwager J., Mikoryak C.A., Steiner L.A.; Mikoryak C.A.; Steiner L.A.; Mikoryak C.A.; Steiner E.A.; Stei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleost
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IG HEAVY CHAIN V REGION XIG14. IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-SEP-2003 (Rel. 47, Last annotation update)
19 heavy chain V region XIG14 precursor (Fragment).
Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.1%; Score 338; DB 1;
50.7%; Pred. No. 5.7e-26;
iive 20; Mismatches 44;
                                                                                                                                                                                                                                                                       EMBL, J03632; AAA49791.1; -...
PIR; B31933; B31933.
HSSP; P01810; ZFBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR00306; Ig_MHC.
InterPro; IPR003596; Ig_V.
InterPro; IPR003596; Ig_V.
IREPRO; IPR003596; Ig_V.
IREPRO; IPR003596; Ig_V.
IREPRO; IREPRO; IGV.
INTERPROSITE; PSS0835; IG_LIKE; 1.
IMMUNOGIObulin V. region; Signal.
NON_TER
                                                                                                                                                                                                                                      121 ----TTAMDYWGQGTSVTVSS 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                  HV02_XENLA
P20957;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 PGKGLEWLGTIWGNGSTDYNSTLKSRLTITKDNSKSQVFLKMNSLQTDDTARYYCASVSI 119
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                                                                                                                                                                                                                                                                                                                                                                                                          11; Gaps
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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-Mul-1999 (Rel. 38, Last annotation update)
19 heavy chain VII region ARH-77 precursor.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                     IG HEAVY CHAIN V REGION MOPC 141. IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                    Length 144;
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                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                            15759 MW; 8E47A7CB3706D30A CRC64;
                                                                                                                                                                                                                                                                                                                                              53.6%; Score 384.5; DB 1;
56.2%; Pred. No. 2e-30;
iive 22; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 YYYGRS-DKYFTLDYWGQGTSVTVSS 144
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                                                        Pfam, PF00047; ig; i. --
SMART, SM0406; IGv; i.
PROSITE, PS50835; IG LIKE; I.
Immunoglobulin V region; Signal.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                          82; Conservative
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                                                                                                                                                                                                                                                                                               144 AA;
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Best Local Similarity
Matches 80; Conserv
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        DR ROBERT LEE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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               20 VQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMGYISYSGITTYN 79
                                   61 TPLRSRVTMLVDTSKNQFSLRLSSVTAADTAVYYCARNLI-AGCIDVWGQGSLVTVSS 117
                                                                                             PSLKSRISITRDTSKNOFFLQLNSVTTGDTSTYYCARSLARTTAMDYWGOGTSVTVSS 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=81012133; PubMed=6774258; Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.; Turosawa Y., Roeder W., Tonegawa S.; Turosawa Y., Roeder W., Tonegawa S.; Turosawa Y., Roeder W., Tonegawa S.; Turo types of sometic recombination are necessary for the generation of complete immunoglobulin heavy-chain genes.";
                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
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IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115 AA; 12447 MW; 7569DD4A4843D500 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.0%; Score 330; DB 1;
57.8%; Pred. No. 2.8e-25;
tive 19; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00406; ĬĠv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal; 3D-structure.
                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
11-SEP-2003 (Rel. 42, Last annotation update)
1g heavy chain V region PJ14 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; V00767; CAA24148.1; -.
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                                                                                                                                                                                                                           STANDARD;
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>115
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PDB; 1G7I; 17-JAN-01.
PDB; 1G7J; 17-JAN-01.
PDB; 1G7M; 17-JAN-01.
PDB; 43C9; 24-JUL-02.
PDB; 43C9; 24-JUL-02.
                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
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                                                                                                                                                                                                                         HV44 MOUSE
P01820;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=78066916; Pubmed=618887; Saul F.A., Amzel L.M., Poljak R.J.;

"Preliminary refinement and structural analysis of the Fab fragment from human immunoglobulin new at 2.0-A resolution.";

J. Biol. Cham. 253:585-597(1978).

-i- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGGI MYELOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Piam; Froust, +3, -.
SMART; 2800406; IGV. 1.
Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.
DOMAIN 1 111 FYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5;
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                                                                                                                                                                                                                                                                                                                                      SEQUENCE.
MEDLINE=77242302; PubMed=407927;
Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.;
Amino acid sequence of the VH region of a human myeloma immunoglobulin (IgG New).";
Biochemistry 16:3412-3420(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: Contains 1 immunoglobulin-like domain. PIR; A90404; GIHUNM. PDB; 7PAB; 31-JAN-94. GJHUNM. GO; GO: 000576; C: extracellular; NAS. GO; GO: 000576; P: extracellular; NAS. GO; GO: 0003923; P: antigen binding activity; NAS. GO; GO: 0006955; P: immune response; NAS. InterPro; IPR07110; Ig-11ke. InterPro; IPR07110; Ig-11ke. InterPro; IPR07156; Ig-NC. InterPro; IPR07156; Ig-V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.9%; Score 337; DB 1;
55.1%; Pred. No. 6.1e-26;
iive 25; Mismatches. 26,
                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ign heavy chain V-II region NEWM.
                                                                                                                                  117 AA
124 MDYWGQGTSVTVSS 137
                     122 FDYWGQGTMVTVTS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 55.1
Matches 65; Conservative
                                                                                                                                STANDARD;
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                                                                                                                                HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VILKENGPILVKPTETLILTCTLSGLSLTTDGVAVGWIRQGPGRALEWLAWLLYWDDDKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 VQLQESGPVLVKPSQSLSLTCTVTGYSITSDH-AWSWIRQFPGNKLEWMGYISY-SGITT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 YNPSLKSRISITRDISKNOFFLQLNSVTTGDISTYYCARSLARTTAMDYWGQGTSVTVSS
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MEDLINE=82075900; PubMed=6273429;
Kataoka T., Nikaido T., Miyata T., Moriwaki K., Honjo T.;
"The nucleotide sequences of rearranged and germline immunoglobulin VH genes of a mouse myeloma MC101 and evolution of VH genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metaza, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. NCBI_TaxID=10090;
                                                        Cunningham B.A., Pflumm M.N., Rutishauser U., Edelman G.M.; "Subgroups of amino acid sequences in the variable regions of immunoglobulin heavy chains."; Proc. Natl. Acad. Sci. U.S.A. 64:997-1003(1969).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.0%; Score 323; DB 1; Length 121; 52.5%; Pred. No. 1.4e-24; ive 22; Mismatches 33; Indels
                                                                                                                                                                                                                                      -:- SIMILARITY: Contains 1 immunoglobulin-like domain.
PTR: A02093; G1HUHE.
RESP: P01825; 7FAB.
G0; G0:0005526; C:extracellular; NAS.
G0; G0:0005953; F:antigen binding activity; NAS.
G0; G0:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR00306; Ig-MHC.
RinterPro; IPR00306; Ig-MHC.
RinterPro; IPR00306; Ig-W.
RinterPro; IPR003596; Ig-V.
RinterPro; IPR0047; ig: I.
SMART; SW00406; IGV: I.
SMART; SW00406; IGV: I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic acid.
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(Rel. 01, Last sequence update)
(Rel. 42, Last annotation update)
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15-SEP-2003 (Rel. 42, Last annotation up
1g heavy chain V region MC101 precursor.
Mus musculus (Mouse).
                                     MEDLINE=70114712; PubMed=5264153;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63; Conservative
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20 VOLQESGPVLVKPSQSLSLTCTVTGYSI-TSDHAWSWIRQFPGNKLEWMGYISYSGITTY
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
1g heavy chain V-II region HE.
Homo saplans (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=82222235; PubMed=6806818;
Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.;
Tomblete amino acid sequence of the delta heavy chain of human immunoglobulin D.";
Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).
-: MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
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PIR; A02099; D2HUWA.
HSSP; P01825; 7FAB.
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GlycosuiteDB; PO1824; --
GlycosuiteDB; PO1824; --
GO; GO:0005876; C:extracellular; NAS.
GO; GO:0005875; F:antigen binding activity; NAS.
GO; GO:000585; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig-MHC.
InterPro; IPR003596; Ig-V.
Pfam; PF0047; ig: 1.
PROSITE; PS50835; IG-LIKE; 1.
Immunglobulin V region.
                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Homo sapiens (Human).
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Matches 66; Conservative
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129 AA;
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P01818;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
19 heavy chain V region XIG8 precursor (Fragment).
Xenopus laevis (African clawed frog).
Edkaryotes, Metszoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
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44.0%; Score 316; DB 1; Length 116;
Best Local Similarity 53.8%; Pred. No. 6.5e-24;
Matches 63; Conservative 22; Mismatches 30; Indels
                                                                                                                                                                                                                              IG HEAVY CHAIN V REGION MC101, IG-LIKE.
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Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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PIR; A31933; A31933.
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InterPro; IPR007110; Ig-like.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
NON TER.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Ffam; PF00047; ig; 1.
SNART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
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128
136
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P20956;
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64 LEWMGYISYSGITTYNPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLARTTA 123
                                                                                                                                                                               62 LEWIGVVRTDGSTAIADSLKNRVTITKDNGKKQVYLQMNGMEVKDTAMYYCTSTLAGTAG 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 NPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLARTTAMDYWGQGTSVTVSS 137
                                                                                                 4 IFVIFMFFSPSCILSQT-LQESGPGTVKPSESLRLTCTVSGFELTSYYVY-WIRQPPRKT
                                                                             4 LILLWLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VTLRESGPALVRPTQTLTLTCTFSGFSLSGETMCVAWIRQPPGEALEWLAWDILNDDKYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 VQLQESGPVLVKPSQSLSLTCTVTGYSITSD-HAWSWIRQFPGNKLEWMGYISYSGITTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE.

MEDILNE=70258837; PubMed=5449120;

Press E.M., Hogg N.M.;

"The amino acid sequences of the Fd fragments of two human gamma-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
7
                                      .3;
    Length 136;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYRROLIDONE CARBOXYLIC ACID.
                                      Indels
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119 AA; 13045 MW; 4E13E00214BAD789 CRC64;
43.5%; Score 312.5; DB 1;
llarity 47.4%; Pred. No. 1.7e-23;
Conservative 26; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
11-SEP-2003 (Rel. 42, Last annotation update)
19 heavy chain V-II region DAW.
                                                                                                                                                                                                                                                                                                                                                                               119 AA
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                                                                                                                                                                                                                                                                                                                                                                               PRT;
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122 YFEHWGOGTMVTVTS 136
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                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                    Similarity
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P01816;
                                      64;
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(USPTO) NNAJB 3DA9 21HT

musculu musculu

sapien

sapien

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Run on:

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MKVLSLLYLLTA1PG1LSDVQLQESGPGLVKPSQSLSLTCSVTGYS1TSGYYWNWIRQFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 74.0%; Score 531; DB 11; Length 479; Best Local Similarity 73.9%; Pred. No. 3.8e-46; Matches 105; Conservative 11; Mismatches 14; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SECUENCE FROM N.A.
Straubberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002091; AAH02091.1; -
HSSP; P01810; 2FBJ.
InterPro; IPR0071006; Ig_MRC.
InterPro; IPR003006; Ig_MRC.
InterPro; IPR003596; Ig_V.
Pfam; PF0047; ig; 4.
SWART; SM04066; IG_V.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50839; IG_LIKE; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
SEQUENCE 479 AA; 51992 MW; 768E39A138918892 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 52.0 kBa protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      479 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
091WR1
099KA4
099KA6
098KA7
088CX7
08WU3
091Z05
091Z05
091Z05
091Z05
099LQ0
099
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092401
090L91
08VCV5
090XF0
0920E7
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Q8VEA0
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Q91XE1
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40.7
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Q99M22
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                                                                                                                                                October 22, 2003, 22:13:15; Search time 62.7917 Seconds (without alignments) 563.024 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                               718
1 MRVLILLWLFTAFPGILSDV......LARTTAMDYWGQGTSVTVSS 137
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                  GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                               830525 seqs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                            OM protein - protein search, using sw model
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096KX8
096KX8
096L73
095973
0950B8
08WIX4
09BU10
09BU10
099KQ4
099KQ4
099KQ4
099KQ4
099KQ4
099KQ4
099KQ4
099KQ4
099KQ4
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sp_human:*
sp_human:*
sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_phage:*
sp_plant:*
sp_plant:*
sp_vodent:*
sp_vodent:*
sp_vortebrate:*
sp_vortebrate:*
sp_vortebrate:*
sp_vortebrate:*
sp_vortebrate:*
sp_vortebrate:*
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Gapop 10.0 , Gapext 0.5
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sp_bacteriap:*
sp_archeap:*
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Maximum DB seq length: 2000000000
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sp_bacteria:*
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1119
150
597
588
597
618
                                         Copyright
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Match
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393.5
386.5
374.5
368
368
368
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368
368
389.5
338.5
3123.5
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                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database
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GNKLEWMGYINYDGSNNYNPSLKNRISITRDTSKNQFFLKLNSVTTEDTATYYCA---- 115

GNKLEWMGYISYSGITTYNPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLAR 120

61

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sapien musculu

sapien

So.

Result

sapien

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PROSITE, PS50835; IG_LIKE; 4. PROSITE; PS00290; IG_MHC; 1. Hypothetical protein. SEQUENCE 496 AA, 53391 MM;
                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=B-cell;
                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                              Query Match
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                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MRVLILLMLFTAFPG-ILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQF 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Hypothetical protein.
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria, Primates; Catarrhini, Hominidee; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                     5.
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 57.7%; Score 414; DB 11; Length 482; Best Local Similarity 60.9%; Pred. No. 4e-34; Matches 84; Conservative 19; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE=Lung;
Strausberg N.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
BMBL, BC016369; AAH161639.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003306; Ig_MHC.
InterPro; IPR073369; Ig_WHC.
Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUB=Colon;
Strauberg R.;
Submitted (ULL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011181; AAH11181.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR003596; Ig_W.
                                                                                                                                                                                                                                                                                                                                               SMART; SM00406; ĪGv; 1.
PROSITE; PSS0835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; 2.
SEQUENCE 482 AA; Ī1865 MW; 312E01F9C1BC7F3C CRC64;
                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 496 AA
                                                                                                   482 AA
               121 TTAMDY-----WGQGTSVTVSS 137
                                     116 --SRGYSWFPNWGQGTLVTVSA 135
                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                               Unknown (Protein for MGC:18822).
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                                                                                                  PRELIMINARY;
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Q96KX8
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62 NKLEWMGYISYSGITTYNPSLKSRISITRDTSKNOFFLQLNSVTTGDTSTYYCAR----S 117
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                                                                                                                                                                                                                                                                                          Gaps
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Mammalia, Eutheria, Primatés, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                 ch 54.8%; Score 393.5; DB 4; Length 496; 1 Similarity 60.0%; Pred. No. 5.3e-32; 84; Conservative 16; Mismatches 31; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 53.8%; Score 386.5; DB 4; Length 613; l Similarity 61.3%; Pred. No. 3.6e-31; 84; Conservative 15; Mismatches 31; Indels 7;
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011857; AAH11857.1; -
InterPro; IPR07110; Ig-11ke.
InterPro; IPR003006; Ig-MHC.
InterPro; IPR003596; Ig-V.
Ffam; PR00047; igj; S.
SWART; SMO0406; Igv; 1.
PROSITE; PS00835; IG_LIKE; S.
PROSITE; PS00290; IG_MHC; 3.
al procein.
496 AA; 53391 MW; D346929849040D69 CRC64;
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SEQUENCE 613 AA, 67273 MW, 31214203FBB421E7 CRC64;
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Last annotation update)
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09UL73
ID 09UL73;
AC 09UL73;
C 09UL73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 SGRTGAIDYWGQGTLVTVSS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 LARTTAMDYWGOGTSVTVSS 137
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Length 150;

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NCBI_TaxID=9606
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    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 VOLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMGYISYSGITTYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                       'Myosin-reactive autoantibodies in rheumatic carditis and normal
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"Clonal proliferation of IgM secreting B cell in the synovium of Behoet's patient with arthritis.";

Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AF103795; AAC79084.1; -.

HSSP; PO1825; AAC79084.1; -.

InterPro; IPR007110; Ig-like.

InterPro; IPR003006; Ig-MC.
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VH4 HEAVY CHAIN VARIABLE REGION.
                                                                                                                                                                                         Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 119;
                   Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;; Score 382; DB 4; Length 11;
;; Pred. No. 1.4e-31;
12; Mismatches 26; Indels
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
VH4 heavy chain variable region precursor (Fragment)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                        fetus.";

Clin. Immunol. Immunopathol. 87:184-192(1998).

EMBL; AF035041; AAD56277.1;

HSSP; PO1825, 7FAB.

InterPro; IPR007110; Ig-like.

InterPro; IPR003006; Ig MHC.

InterPro; IPR003596; Ig-V.

Fam; PP00047; ig; 1.

SMART; SM0046; IGv; 1.
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                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=98277139; PubMed=9614934;
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PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.2%;
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Query Match

Best Local Similarity 66.4%,

Conservative 79; Conservative 79;
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SMART; SM00406; IGv; 1
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                                                             Homo sapiens (Human)
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01-MAR-2003
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NON TER
SEQUENCE
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SEQUENCE
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63 GLEWIGEINHSGITNYNPSLKSRVTISVDTSKRQLSLKLSSVNAADTAVYXCARVITRAS 122
                                                                                                                                                                                                                                               64 KGLEWIGSLHNSGSDYYNPSLKSRVTISVDTSKNQPSLRLSSVTAADTAVYYCAR--LGM 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 KLEWMGYISYSGITTYNPSLKSRISITRDISKNOPFLOLNSVTTGDISTYYCARSLARTT 122
                                                                                                                                                                                                                     62 NKLEWMGYISYSGITTYNPSLKSRISITRDTSKNOFFLQLNSVTTGDTSTYYCARSLART 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
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                                                                                                                                       4 LWFFLLLVAAPRWVLSQLQLQESGPGLVKPSETLSLSCTVSGGSISSTNYYWGWIRQPPE
                                                                                                          7 LWLF---TAFP-GILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITS-DHAWSWIRQFPG
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01-JUN 2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                     7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 52.1%; Score 374; DB 4; Length 597; Local Similarity 56.3%; Pred. No. 6.7e-30; Local Substructive 18; Mismatches 32; Indels 1
                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.; Strausberg R.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC006180; AAH01872.1; -. EMBL; BC001872; AAH01872.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR007110; Ig-like.
InterPro; IPR003106; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 5.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS00290; IG_MHC; 3.
Hypochetical protein.
SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last annotation update)
52.2%; Score 374.5; DB 4;
58.8%; Pred. No. 1.1e-30;
ive 18; Mismatches 31;
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TISSUE=Muscle, and Lymph;
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01-MAR-2002 (TrEMBLrel, 2)
01-MAR-2003 (TrEMBLrel, 2)
Hypothetical protein.
Homo sapiens (Human).
                            Best Local Similarity 58.8
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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63 KLEWMGYISYSGITTYNPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLARTT 122
                                                                                                                                                                                                                                             618 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 -----AMDYWGQGTSVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 PGTDGRYGMDVWGQGTTVTVSS 144
                                                                                          ------AMDYWGQGTSVTVSS 137
                                                                                                                                123 PGTDGRYGMDVWĠQĠŤTVŤVSS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART, SM00406; ĬĠv; 1.
PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS00290; IG_MHC; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single chain Fv (Fragment) Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Lymph;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                    096AA6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 GLEWIGEINHSGSTNYNPSLKSRVTISVDTSKKQLSLKLSSVNAADTAVYYCARVITRAS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 LWLF---TAFP-GILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Length 588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL, EC002963; AAH02963.1; -- HSSP; P01825; 7FAB.
                                                                                                                              Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases:
EMBL; BC019235; AAH19235.1;
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                       al protein.
588 AA; 64438 MW; FC60DBAD82B39FD7 CRC64;
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597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUNAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
51.3%; Score 368; DB 4;
Best Local Similarity 55.6%; Pred. No. 2.7e-29;
Matches 79; Conservative 18; Mismatches 33;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_W.
Pfam; PF00047; ig; 5.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                             Pfam; PF00047; 1g; 5.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 5.
PROSITE; PS00290; IG MHC; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART, SM00406, IGV; 1.
PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS00290; IG_MHC; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                       Hypothetical
SEQUENCE 58
                                                                                                            TISSUE=Lymph;
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Q9BU10;
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63 KLEWMGYISYSGITTYNPSLKSRISITRDTSKNOPFLQLNSVTTGDTSTYYCARSLARTT 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=BALB/C;
MPDILINE=98169018; PubMed=9510199;
Hawlisch H., Frank R., Hennecke M., Baensch M., Sohns B., Arseniev L.,
Bautsch W., Kola A., Klos A., Koehl J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 LWLF---TAFP-GILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGN
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Evbaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 51.3%; Score 368; DB 4; Length 618; Local Similarity 55.6%; Pred. No. 2.9e-29; es 79; Conservative 18; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg W. Strausberg M. Strausberg M. Strausberg M. Strausberg M. Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. EMBL, BC017356, AM17056.1; -. InterPro; IPR0071010; Ig-like. InterPro; IPR007006; Ig_MHC. InterPro; IPR007596; Ig_W. Pfam; PF00047; Ig'S SMART; SM00406; IGv; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
SEQUENCE 618 AA; 67758 MW, 96DBD4C7C696E0A6 CRC64;
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Last annotation update)
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473 AA
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                                                                                                                                                                                                                                                                   EMBL, BC025985; AAH25985.1; --
InterPro; IRR000923; BlueCu 1.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR00306; Ig-MHC.
InterPro; IPR003596; Ig-MHC.
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NON TER 1 1 1
NON_TER 130
                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00196; COPPER BLUE PROSITE; PS50835; IG LIKE; 4. PROSITE; PS00290; IG_MHC; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 TAMDYWGQGTSVTVS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 GFGAHWGQGKLVSVS 145
                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 51.1%
Matches 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1
                                                                                                                                                                                                           [1] SEQUENCE FROM N.A.
TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
 137 S 137
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                        122
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                                                                                   Q8TC63
                                                            RESULT 13
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                                                                                                                                                                                                                                                                                                 77 TYNPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLARTTAMDYWGQGTSVTVS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 PSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLAR--TTAMDYWGQGTSVTVSS 137
                                                                                                                                                                                                                                                 2 VQLKESGPGLVAPSQSLSITCTVSGFPLTS-HGVSWVRQPPGKGLEWLGVIWGDGNTKYH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 VQLQESGPVLVKPSQSLSLTCTVTGYSITSDH-AWSWIRQFPGNKLEWMG--YISYSGIT 76
                                                                                                                                                                                                                                  20 VOLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMGYISYSGITTYN 79
 "Site-Directed C3a-Receptor Antibodies from Phage Display Libraries.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VOLOOSGPGLVKPSQTLSLTCAISGDSVSSNSAAWNWIROSPSRGLEWLGRTYYRSKWYN
                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3,
                                                                                                                                                                                    DB 11; Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32; Indels
                                                                                                                                                                                51.2%; Score 367.5; DB 11; Length 62.5%; Pred. No. 4.5e-30; ive 17; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 AA; 13719 MW; 56CB0612586A6529 CRC64;
                                                                                                                                                          121 AA; 13255 MW; D293E4EBC8C59D5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035039; AAD56275.1; -.
HSSP; PO1825; 774B.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003586; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM06406; IGy. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          th Soniarity 50.1%; Score 359.5; DB Similarity 61.2%; Pred. No. 3e-29; 74; Conservative 12; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                        122 AA
        J. Immunol. 160:2947-2958(1998).
EMBL, AJ722590; CAA10890.1; -.
HSSP, PO1825; 7FAB.
InterPro; 1PR00110; Ig-like.
InterPro; 1PR003506; Ig_MHC.
InterPro; 1PR003596; Ig_V.
Ffam, PF00047; ig; 1.
Ffam, PF00047; ig; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                             Local Similarity
les 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                (Fragment)
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SEQUENCE
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                                                                                                                        Plasmid
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62 NKLEWMGYISYSGITTYNPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLART 121
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"Isolation and Sequence Analysis of Monoclonal Anti-Histone and Anti-Thyroglobulin Single Chain Fv from SLE Patient by Phage Display.";
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.9%; Score 336.5; DB 4; Length 473; 51.1%; Pred. No. 3.6e-26; ive 25; Mismatches 36; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Anti-thyroglobulin heavy chain variable region (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;
QBTC63;
01-UNM-2002 (TrEMBLrel. 21, Created)
01-UNM-2002 (TrEMBLrel. 21, Last sequence update)
10-UNM-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Homo sapiens (Human)
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77 ---TYNPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLART-----TAMDYWG 128
                                                                                                                                                                                               79 NPSLKSRISITRDISKNOFFLQLNSVITGDISTYYCA-RSLARTTAMDYWGQGISVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VQLQQSGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQSPGKGLEWIGSLYYSGSTYS 61
                                                                                                        20 VOLQESGPVLVKPSQSLSLTCTVTGYSI-TSDHAWSWIRQFPGNKLEWMGYISYSGIT-- 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                      11;
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                               Query Match
45.8%; Score 328.5; DB 4; Length 130;
Best Local Similarity 55.0%; Pred. No. 5e-26;
Matches 71; Conservative 16; Mismatches 31; Indels 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEGUENCE FROM N.A.
SEGUENCE FROM N.A.
MU X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
43.6%; Score 313; DB 4; Length 121;
Best Local Similarity 54.2%; Pred. No. 1.8e-24;
Matches 65; Conservative 17; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
130 AA; 13901 MW; 036131FC6EC1551E CRC64;
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121 AA; 13695 MW; D582D450596BDD35 CRC64;
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EMBL; AF035018; AAD56254.1; -.
HSSP; P01825; 7PAB.
InterPro; IPR07110; Ig-11ke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                              121 AA
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                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TYEWBLrel. 13, Created)
01-MAY-2000 (TYEWBLrel. 13, Last seq
01-MAR-2003 (TYEWBLrel. 23, Last ann
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
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                    (without alignments)
398.931 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                               October 22, 2003; 22:14:35 ; Search time 14.5303 Seconds
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1 MRVLILLWLFTAFPGILSDV......LARTTAMDYWGQGTSVTVSS
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/cgn2_6/ptodata/2/iaa/SB_COMB.pep:*
/cgn2_6/ptodata/2/iaa/AA_COMB.pep:*
/cgn2_6/ptodata/2/iaa/AB_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-137-1170-69
US-08-466-1128-18
US-08-466-151-5
US-08-466-163B-5
US-08-466-163B-5
US-08-137-1170-64
US-08-11-080-23
US-08-211-080-23
US-08-211-080-23
                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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US-08-308-494A-13
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US-09-065-059-11
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US-08-082-842A-5
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Maximum Match 100%
Listing first 45 summaries
                                          - protein search, using sw model
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Maximum DB seq length: 200000000
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Match Length
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478.5
478.5
468.5
468.5
468.4
468
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Sequence 114, App
Sequence 103, App
Sequence 110, App
Sequence 2, Appli
Sequence 2, Appli
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    US-08-672-345C-10
US-08-672-345C-11
US-08-672-345C-101
US-09-214-095D-110
US-09-214-095D-110
US-09-214-095D-105
US-09-214-095D-105
US-08-672-345C-12
                                                                      US-09-214-095D-114
US-08-672-345C-103
US-09-214-095D-110
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ALIGNMENTS

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APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BANDIG, Mary
APPLICANT: BRNDIG, Mary
APPLICANT: BRNDIG, Mary
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 2000-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION NUMBER: US 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION NUMBER: US 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION NUMBER: US 4-32084
FILING DATE: 25-APR-1991
ATPONEY/AGENT INFORMATION:
ANAME: MERNED JAYONA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
; Sequence 31, Application US/08137117D
; Patent No. 5795965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 31:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (202) 672-5399
                                              GENERAL INFORMATION:
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61 GNKLEWMGYISYSGITTYNPSLKSRISITRDISKNOFFLOLNSVITGDTSTYYCARSLAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GNKLEWMGYISYSGITTYNPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYCARSLAR 120
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Parent No. 5795965
GENERAL INFORMATION:
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: SALDANHA, Jose
ITILE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Flopped disk
MEDIUM TYPE: Flopped disk
MEDIUM TYPE: Flopped disk
COMPUTER: IBM PC compatible
CONFUNENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 2-FEB-1992
FILING DATE: 19-FEB-1992
FILING DATE: 25-FEB-1992
ATTOMNOMBER: UP 3-95476
FILING DATE: 25-APR-1991
ATTOMNOMBER: UNFORMATION:
ANNOWER: APPLICATION NUMBER: UP 3-95476
FILING DATE: 25-APR-1991
                                                                                                                                          Query Match 100.0%; Score 718; DB 2; Best Local Similarity 100.0%; Pred. No. 1.2e-65; Matches 137; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 TTAMDYWGQGTSVTVSS 137
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                         , MOLECULE TYPE: protein US-08-436-717-31
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Pred. No. 1.2e-65;
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Patent No. 5817790
GENERAL INFORMATION
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: BENDIG, Mary
APPLICANT: BENDIG, Mary
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INFERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                        Indels
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CITY: Washington
STATE: 0.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDLUM TYPE: FIDPDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTING NATES
SOFTWARE: DATES NATES
SOFTWARE: DATES NATES NATE
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR.1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA: JP 4-32084
FILING DATE: 19-FEB-1992
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INPORMATION:
NAME: WEGNER, HAROID C.
REGISTRATION NUMBER: 25,258
REGISTRATION NUMBER: 25,258
REGISTRATION NUMBER: 25,258
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5309
                                                                                                                                             Query Match
100.0%; Score 718; Di
Best Local Similarity 100.0%; Pred. No. 1.28
Matches 137; Conservative 0; Mismatches
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INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
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amino acid
                                         ; MOLECULE TYPE: protein US-08-137-117D-31
TOPOLOGY: linear
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66 EWIGYISYSGITTYNPSLKSRVTMLRDTSKNQFSLRLSSVTAADTAVYYCARSLARTTAM 125
                                                                                                                                                                                                                                              65 EWMGYISYSGITTYNPSLKSRISITRDISKNOFFLOLNSVITGDISTYYCARSLARTTAM 124
                                                                                                                                                                       5 ILLWLFTAFPGILSDVQLQESGPVLVKPSQSLSLTTVTGYSITSDHAWSWIRQFPGNKL 64
                                                                                                Gaps
                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt STREET: 3100 No. 6111079west Center, 90 South Seventh St CITY: Minneapolis
                                           Length 138;
                                                                                             17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: LOPEZ, OSVALDO
APPLICANT: MURRAY, PETER JOSEPH
APPLICANT: GOEBEL, PETER
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                             74.9%; Score 538; DB 2; 75.9%; Pred. No. 2.2e-47;
                                             Query Match 74.9%; Score 538; DB 3
Best Local Similarity 75.9%; Pred. No. 2.2e-4
Matches 101; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 04-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEN Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 18, Application US/08767128; Patent No. G111079
GENERAL INFORMATION:
APPLICANT: WYLIE, DWANE E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 80
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                          126 DYWGQGSLVTVSS 138
                                                                                                                                                                                                                                                                                                                                         125 DYWGQGTSVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
US-08-767-128-18
US-08-436-717-69
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                                                                                                                                                                                                                                                                          66 EWIGYISYSGITTYNPSLKSRVTMLRDTSKNQFSLRLSSVTAADTAVYYCARSLARTTAM 125
                                                                                                                                             5 ILLWLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKL 64
                                                                                                                                                                       6 IILFLVATATGVHSQVQLQESGPGLVRPSQTLSLTCTVSGYSITSDHAMSWVRQPPGRGL 65
                                           74.9%; Score 538; DB 1; Length 138; 75.9%; Pred. No. 2.2e-47; tive 15; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: BALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
FILING DATE: 24-APR-1992
FILING DATE: 19-FEB-1992
PRIOR APPLICATION NUMBER: UP 4-32084
FILING DATE: 19-FEB-1992
APPLICATION NUMBER: UP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, HAION C.
REGISTRATION NUMBER: 25,258
REGISTRATION NUMBER: 25,258
REGISTRATION NUMBER: 25,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53466/126/AAOK
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3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 69, Application US/08436717
Patent No. 5817790
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 53
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5399
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                       111||: |||||
126 DYWGQGSLVTVSS 138
                                                                                                                                                                                                                                                                                                                                         125 DYWGOGTSVTVSS 137
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TYPE: amino acid
TOPOLOGY: linear
                                             Query Match
Best Local Similarity 75.9%
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington
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ZIP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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STREET: 300
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US-08-137-117D-69
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US-08-436-717-69
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Query Match
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                                                                                                                                                                                                                                                                                                                                                         61 NPSLKSRISITRDISKNOFFLQLNSVTTEDTATYYCARCGNYPWYFDYWGQGTTLTVSS 119
                                                                                                                                                                                                                                                                 1 DVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGNKLEWMGY1SYSGSTSY
                                                                                                                                                                                                                                        19 DVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMGYISYSGITTY
                                                                                                                                                                                                     Gaps
                                                                                                                                                             Length 119;
                                                                                                                                                                                                   Indels
                                                                                                                                                           74.4%; Score 534; DB 3;
85.7%; Pred. No. 4.7e-47;
iive 6; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible SOFRATING SYSTEM PC-DOS/MS-DOS SOFWARE: WinPatin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,151
FLING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/08466151
Patent No. 6037453
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 39,044
REGISTRATION NUMBER: 39,044
REPERENCE/DOCKET NUMBER: P0718P2C1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/405617
PILING DATE: 15-MAR.1995
PRIOR APPLICATION DATA: 08/185899
FILING DATE: 26-JAN-1994
PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/879495
FILING DATE: 07-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/466163
FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/405617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genentech, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
              MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-767-128-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 130 amino acids
Amino Acid
                                                                                                                                                                              Best Local Similarity 85.73
Matches 102, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DNA Way
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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79 NPSLKSRISITRDTSKNOFFLQLNSVTTGDTSTYYCARSLARTTAMDYWGQGTSVTVSS 137
                                                                                                                                                                                                                                   61 NPSLKSRISITRDTSKNOFFLQLNSVTTEDTATYYCAWVVA--YAMDYWGQGTSVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 NPSLKSRISITRDISKNQFFLQLNSVTTEDTATYXCAWVVA--YAMDYWGQGTSVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79 NPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLARTTAMDYWGQGTSVTVSS 137
                                                                                                                               1 DVQLQESGPGLVKPSQSLSLTCTVTGYTITSDNAWNWIRQFPGNKLEWMGYINHSGTTSY
                                                                                                      19 DVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMGYISYSGITTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DVQLQESGPGLVKPSQSLSLTCTVTGYTITSDNAWNWIRQFPGNKLEWMGYINHSGTTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 DVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMGYISYSGITTY
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                                                          5
Score 534; DB 3; Length 130;
Pred. No. 5.3e-47;
8; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 534; DB 4; Length 130;
Pred. No. 5.3e-47;
8; Mismatches 6; Indels
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Patent No. 5795965

GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: ALDANIA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INC. 0.4.29.09.
GENERAL INFORMATION:
APPLICANT: Oracleu, Paula M.
APPLICANT: Preste, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: PO718P2C1D1
CURRENT APPLICATION NUMBER: US/08/466,163B
CURRENT FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR PILING DATE: 1994-01-26
PRIOR PILING DATE: 1995-03-15
PRIOR FILING DATE: 1994-01-76
PRIOR FILING DATE: 1991-08-14
SEQ ID NO SEQ ID NOS: 64
SEQ ID NO SEQ ID NOS: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/08466163B Patent No. 6329509
       74.48;
86.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74.4%;
86.6%;
                              Best Local Similarity 86.69
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 86.6
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20007-5109
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61 ITTYNPSLKSRVTWLRDTSKNQFSLRLSSVTAADTAVYYCARSLARTTAMDYWGQGSLVT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/07956399;
Patent No. 587617;
GENERAL INPOWARTION:
APPLICANT: SHIMANIRA, TOSHIRO
APPLICANT: TAKI, SHINSUKE
APPLICANT: APPLICANT: APPLICANT
APPLICAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BINDING TO HEAVY
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73.4%; Score 527; DB 2; Length 12
Best Local Similarity 79.7%; Pred. No. 2.5e-46;
Matches 98; Conservative 13; Mismatches 12; Indels
       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                      SOFTWARE: PAREAGIN RELEASE #1.0, Version #1
SUPPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
FILING DATE:
CLASSIFCATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, HATOLIO C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53,466/126/AAOK
TELEPRAN: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 123 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1755 S. Jeffer
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: protein US-08-436-717-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 GILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMGYISYSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 64, Application US/08436717

Batent No. 5817790

GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Maeayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: BENDIG, Mary
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INFERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE:
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/137,117D FILING DATE: 0.0-DEC-1993 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTONNEY/AGENT INFORMATION:
NAME: WEGNER, HATOLI C.
REGISTRATION NUMBER: 25,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: FOLCY & Lardner STREET: 3000 K Street, N.W., Suite 500 STATE: D.C. COUNTRY
                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 123 amino acids
amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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; MOLECULE TYPE: protein
US-08-137-117D-64
                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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79 NPSLKSRISITRDISKNOFFLOLNSVITGDISTYYCARSLARTTAMDYWGQGTSVTVSS 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                             19 DVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMGYISYSGITTY
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                      ŝ
                                                                                                                                                                                                                                                                                                                     Query Match 69.7%; Score 500.5; DB 1; Length 114; Best Local Similarity 81.5%; Pred. No. 1.1e-43; Matches 97; Conservative 8; Mismatches 9; Indels 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23, Application US/08211980
Patent No. 5665569
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
TITLE OF INVENTION: HIV Immunotherapeutics
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Borun
APDRESSEE: Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 24-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,457
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: BOLUN, Michael F.
REGISTRATION NUMBER: 25,477
                   TELECOMMUN: (J.L.
TELEPHONE: (J.L.
TELERAX: (312) 474-UT.
TELERAX: 25-3856
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TUBENGTH: 114 amino acids
TUBENGTH: 114 amino acids
TUBENGTH: 111 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION: (312) 474-6300
TELEPHAX: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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US-08-211-980-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 YNPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLARTTAMDYWGQGTSVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 SDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMGYISYSGITT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 518.5; DB 2; Length 2
Pred. No. 4.4e-45;
8; Mismatches 12; Indels
SOFTWARE: PAC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/956,399
FILING DATE: 19921005
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Marshall, O'Toole, Gerstein, Murray ADDRESSEE: Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/111,080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 6300 Sears Tower, 233 S. Wacker Drive CITY: Chicago STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-111-080-23
Sequence 23, Application 08/111080
Sequence 23, Application 08/111080
Patent No FSS8865
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
TITLE OF INVENTION: HIV Immunotherapeutics
WUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                                                    APPLICATION 510
CLASSIPICATION 510
CLASSIPICATION 510
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5876717man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-586-0
TELEPAN: (703) 413-3000
TELEPAN: (703) 413-3200
TELEPAN: (703) 413-3200
TELEPAN: (703) 413-3200
TELEPAN: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LBNGTH: 240 amino acids
TYPE: AMINO ACID
TYPE: AMINO ACID
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RIOR APPLICATION DATA:
APPLICATION NUMBER: 0507/748,562
FILING DATE: 22-ANG-1991
FRIOR APPLICATION DATA:
FILING DATE: 24-ANG-1991
FILING DATE: 24-ANG-1992
PRIOR APPLICATION DATA:
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FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 31629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 82.5%;
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear;
MOLECULE TYPE: protein
US-07-956-399-2
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                                                                                        1 EVQLQESGRGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGNKLEWMGYISYSGSTTY 60
                                                                                                                                                                         61 NPSLKSRISITRDTSKNLFFLQLSSVTSEDTATYYCARG-----SFGDWGQGTLVTVSA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79 NPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLARTTAMDYWGQGTSVTVSS 137
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                                                                                                                                                 79 NPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLARTTAMDYWGQGTSVTVSS 137
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                                                               19 DVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMGYISYSGITTY
                          5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69.7%; Score 500.5; DB 5; Length 114; 81.5%; Pred. No. 1.1e-43; tive 8; Mismatches 9; Indels 5.
81.5%; Pred. No. 1.1e-43;
tive 8; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ohno, Tsuneya
TITLE OF INVENTION: HIV Immunotherapeutics
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray
ADDRESSEE: Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 6300 Sears Tower, 233 S. Wacker Drive CITY: Chicago STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 24-AUG-1992
PRIOR APPLICATION NUMBER: US 08/039,457
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 31629
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                 Sequence 23/ Application PC/TUS9307967 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DECOUNT. (312/
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 69.77
Best Local Similarity 81.5
Matches 97; Conservative
                      97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein PCT-US93-07967-23
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                        Matches
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RESULT 14 US-09-170-769A-2

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APPLICANT: INFORMATION:
APPLICANT: LETURCO, Didier
APPLICANT: LETURCO, Didier
APPLICANT: METATRY, Ann
APPLICANT: METATRY, Ann
APPLICANT: METATRY, Ann
APPLICANT: TOBLAS, Peter
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING CD14 MEDIATED CELL, ACTIVA
FILE REFERENCE: SCRIP1140-3
CURRENT APPLICATION NUMBER: US/09/170,769A
CURRENT FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: US 08/070,160
PRIOR APPLICATION NUMBER: US 08/070,160
PRIOR PILING DATE: 1993-05-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 LELQQSGPGLVKPSQSLSLTCTVTGYSITSDSAWNWIRQFPGNRLEWMGYISYSGSTSYN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 PSLKSRISITRDTSKNOFFLOLNSVTTGDTSTYYCARSLARTTAMDYWGQGTSVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 PSLKSRISITRDTSKNQFFLQLMSVTTEDTATYYCVRGL----RFAYWGKGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 VQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMGYISYSGITTYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 499; DB 4; Length 213;
Pred. No. 3.6e-43;
9; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SEINO, Ken-ichiro
APPLICANT: KAYAGAKI, No. 6068841uhiko
APPLICANT: KAYAGAKI, No. 6068841uhiko
APPLICANT: WAKATA, Hideo
APPLICANT: OKUMREA, Ko-
APPLICANT: NAKATA, Motomi
TITLE OF INVENTION: THERAPEUTIC AGENT FOR HEPATITIS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCDermott, Will & Emery
STREET: 99 Canal Center Plaza
CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/09065059; Patent No. 6068841; GENERAL INFORMATION:
Sequence 2, Application US/09170769A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-42,368
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION TELEPHONE: 703-518-5100 TELEFAX: 703-684-1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: BUCCA Ph.D., Daniel
REGISTRATION NUMBER: P-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRGANISM: Murine US-09-170-769A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-065-059-11
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Search completed: October 22, 2003, 22:20:50 Job time : 15.5303 secs

Sequence 1, Sequence 70,

Sequence 70, Appli Sequence 7, Appli Sequence 7, Appli Sequence 10, Appli Sequence 11, Appl Sequence 102, Appl Sequence 106, Appl Sequence 119, Appl Sequence 119, Appl Sequence 110, Appl Sequence 110, Appl Sequence 110, Appl

Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli

App

Sequence 145, Sequence 5, A Sequence 5, A Sequence 5, A Sequence 7, A Sequence 7, A Sequence 8, A Se

Perfect score:

Run on:

Sequence:

Minimum DB Maximum DB

Database :

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NPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLARTTAMDYWGQGTSVTVSS 137
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Patent No. US20010033842A1

GENERAL INFORMATION:

APPLICANT: Jardieu, Paula M.

APPLICANT: Presta, Leonard G.

TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)

FILE REFERENCE: P0718P2C2US

CURRENT APPLICATION NUMBER: US/09/802,077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 534; DB 9; Length 130;
Pred. No. 3.8e-43;
8; Mismatches 6; Indels
0 US-10-184-300A-1

0 US-09-144-886-70

US-09-802-096-7

US-09-925-179-7

US-09-940-727B-10

US-09-940-727B-10

US-09-940-727B-10

US-09-940-727B-10

US-09-940-727B-10

US-09-940-727B-110

US-09-940-727B-110

US-09-940-727B-110

US-09-940-727B-110

US-09-940-727B-110

US-09-940-727B-110

US-09-940-727B-110

US-09-92-171-2

US-09-92-077-3

US-09-92-171-2

US-09-92-171-2

US-09-92-179-3

US-09-92-179-3

US-09-92-179-3

US-09-92-179-3

US-09-92-179-3

US-09-92-179-3

US-09-92-179-6

US-09-92-179-6

US-09-92-179-6

US-09-97-141-5

US-09-874-141-5

US-09-874-141-7

US-09-874-141-7

US-09-874-141-7

US-09-874-141-7

US-09-874-141-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR PELICATION NUMBER: US 08/405,617
PRIOR PILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR PILING DATE: 1994-01-26
PRIOR PLING DATE: 1992-08-14
PRIOR PELING DATE: 1992-08-14
PRIOR PELING DATE: 1992-05-07
PRIOR PELING DATE: 1992-06-07
PRIOR PELING DATE: 1992-06-07
PRIOR PELING DATE: 1991-08-14
PRIOR FILING DATE: 1991-08-14
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86.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 86.6'
Matches 103; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130
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US-09-802-077-5
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422.5
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Sequence 36, Appl
Sequence 59, Appl
Sequence 53, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Appli
Sequence 258, App
Sequence 13, Appl
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Sequence 5, Appli
Sequence 5, Appli
Sequence 58, Appli
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Sequence 270, App
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902.237 Million cell updates/sec
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Sequence 2, 7
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718
1 MRVLILLWLFTAFPGILSDV.......LARTTAMDYWGQGTSVTVSS 137
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                                                                                                                            October 22, 2003, 22:16:46 ; Search time 25.428 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB_pep:*
2: /cgn2_6/ptodata/2/pubpaa/NCT_NEW_PUB_pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB_pep:*
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7: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB_pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB_pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB_pep:*
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19: /cgn2_6/ptodata/2/pubpaa/USIOC_PUBCOMB_pep:*
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-925-179-5
US-09-144-886-58
US-09-144-886-59
US-09-874-141-53
US-10-184-300A-3
US-10-207-655-270
US-09-858-349-2
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US-09-940-727B-13
US-10-184-300A-2
US-09-874-141-49
                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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US-09-802-096-5
                                                                                                                                                                                                                                                                                                                                  629382 segs, 167460630 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                      OM protein - protein search, using sw model
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length: 2000000000
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Match
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78 9

Sequence 49,

Result No.

Gaps

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Sequence 36, Application US/10310674A
Publication No. US2003166860A1
GENERAL INFORMATION:
APPLICANT: TEGENERO GmbH
TITLE OF INVENTION: Fearly
FILE REPRENCE: 00140/004001
CURRENT APPLICATION MHERR: US/10/310,674A
CURRENT APLICATION MHERR: US/10/310,674A
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 36
LENGTH: 121
LENGTH: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EVQLQESGPGLVKPSQSLSLTCTVTGYSIT-DYAMNWIRQFPGKKLEWMGYISYSGSTGY 59
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                                                                                                                                                                                                                                    79 NPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLARTTAMDYWGQGTSVTVSS 137
                                                                                                                                                                                                                                                                                  61 NPSLKSRISITRDTSKNQFFLQLNSVTTEDTATYYCAWVVA--YAMDYWGQGTSVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 NPSLKSRISITRDISKNOFFLQLNSVTTGDISTYYCARSLARTTAMDYWGQGTSVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 58, Application US/09144886

Parent No. US20020155114A1

GENERAL INFORMATION:
APPLICANT: Marks, James D.
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
FILE REFERENCE: 2500.11710S
CURRENT APPLICANTON NUMBER: US/09/144,886
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 58
LUNGTH: 115
                                                                                                                                                             1 DVQLQESGPGLVKPSQSLSLTCTVTGYTITSDNAWNWIRQFPGNKLEWMGYINHSGTTSY
                                                                                                                               19 DVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMGYISYSGITTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: BoNT/A clone OTHER INFORMATION: 1E8 region VH epitope 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 72.6%; Score 521; DB 10; Length 115; Best Local Similarity 86.6%; Pred. No. 5.7e-42; Matches 103; Conservative 3; Mismatches 9; Indels 4
                     Length 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 121;
                                                                         Indels
                     Score 534; DB 11;
Pred. No. 3.8e-43;
8; Mismatches 6;
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US-10-310-674A-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 521; DB 1;
Pred. No. 6e-42;
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                        74.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                   Best Local Similarity 86.0
Matches 103; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                               US-09-144-886-58
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                             Query Match
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                                                                                                            Sequence 5, Application US/09802096

Patent No. US20010038839A1

GENERAL INPORMATION:
APPLICANT: Jazdieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended TILE OF INVENTION NUMBER: US/09/802,096
CURRENT FILING DATE: 201-03-08
FRIOR PILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR PILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-05-07
PRIOR PILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
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; Publication No. US20030044858A1
; GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Anti-1gE Antibodies (as amended)
FILE REFERENCE: POT18P2C1DICLUS
CURRENT APPLICATION UNMBER: US/09/925,179
FRIOR APPLICATION NUMBER: US 08/466,163
PRIOR APPLICATION NUMBER: US 08/466,163
PRIOR FILING DATE: 1995-06-06
PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-08-14
PRIOR FILING DATE: 1991-08-14
PRIOR FILING DATE: 1991-08-14
PRIOR FILING DATE: 1991-08-14
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 68
SEQ ID NO 5
LENGTH: 130
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Pred. No. 3.8e-43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Mus musculus US-09-802-096-5
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                                                                                                    US-09-802-096-5
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, ORGANISM: Homo sapiens
US-09-874-141-53
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APPLICANT: PAN, LI-ZHEN
APPLICANT: HANNA, NABIL
APPLICANT: HANNA, NABIL
APPLICANT: RASTETTER, WILLIAM H.
APPLICANT: KLOETZER, WILLIAM S.
TITLE OF INVENTION: NON-AGONISTIC ANTIBODIES TO HUMAN GP39, COMPOSITIONS
TITLE OF INVENTION: CONTAINING, AND THERAPEUTIC USE THEREOF
FILE REPERBACKE: 037003-0280632
CURRENT APPLICATION NUMBER: US/09/874,141
CURRENT FILING DATE: 2001-06-06
PRIOR PRIOR DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PATENTIN US: 52.1
SEQ ID NO 53
LENGTH: 140
TYPE: PRT
                                                                                                                             79 NPSLKSRISITRDTSKNOFFLQLNSVTTGDTSTYYCARSLARTT--AMDYWGQGTSVTVS 136
                                                                                                                                                          61 NPSLKSRISITRDTSKNQFFLQLNSVTTEDTATYYCARDWPRPSYWYFDVWGAGTTVTVS 120
                                                                    1 DVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGNKLEWMGYIRYSGSTSY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 DVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMGYISYSGITTY 78
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                                           19 DVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMGYISYSGITTY
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    2; Gaps
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Batent NO. US20020155114A1

GENERAL INFORMATION:
APPLICANT: Marks, James D
APPLICANT: Amersdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Botulinum Neurotoxins
FILE REFERENCE: 2500 117USO
CURRENT APPLICATION UNMERR: US/09/144,886
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
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US-09-144-886-59
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  12; Indels
  6; Mismatches
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SEQ ID NO 59
LENGTH: 115
  101; Conservative
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                                                                                                                   1 MRVLILLWLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFP 60
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                                                                                                                                                     19 DVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMGYISYSGITTY
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APPLICANT: Ledbetter, Martha S.
APPLICANT: Hayden-Ledbetter, Martha S.
FITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069.401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
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   DB 11; Length 140;
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                                                         Indels
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LOCATION: ()..()
OTHER INFORMATION: Synthetic construct of 3B6DIVHv7
71.4%; Score 512.5; DB 11; 75.5%; Pred. No. 4.5e-41; Live 12; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/10184300A
Fublication No. US20030124056A1
GENERAL INFORMATION:
APPLICANT: Carr, Francis J.
APPLICANT: Carr, Francis J.
TITLE OF INVENTION: Carrier molecules
FILE REFERENCE: 229752001700
CURRENT APPLICATION NUMBER: US/10/184,300A
CURRENT FILING DATE: 2002-10-29
PRIOR FILING DATE: 2002-10-26
PRIOR FILING DATE: 2001-0-6
SEQ ID NOS: 12
SEQ ID NOS: 12
SEQ ID NOS: 12
SEQ ID NOS: 13
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Query Match
Best Local Similarity 75.5%
Matches 105; Conservative
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61 NPSLKNRISITRDISKNQFFLKLNSVTTEDTATYYCARXXXXXXXXDYWGQGTTVTVAA 120
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Publication No. US20030118592A1;
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
TILLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS:
FILE REFERENCE: 390069.401C1;
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: PatentIn version 3.0
SEQ ID NO 258
LENGTH: 119
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TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REPERENCE: 0575/51400-B
CURRENT PILLOATION NUMBER: US/09/940,727B
CURRENT PILLING DATE: 2002-09-04
PRIOR FILLING DATE: 1998-12-28
PRIOR FILLING DATE: 1998-12-28
PRIOR FILLING DATE: 1997-06-25
PRIOR FILLING DATE: 1997-06-25
PRIOR FILLING DATE: 1996-06-25
NUMBER OF SEQ ID NOS: 121
                                                                                                                                                     Query Match 69.3%; Score 497.5; DB 9; Best Local Similarity 78.3%; Pred. No. 1.2e-39; Matches 94; Conservative 9; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 68.8%; Score 494; DB 15; Best Local Similarity 79.0%; Pred. No. 2.1e-39; Matches 94; Conservative 10; Mismatches 15;
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SEQ ID NO 13
LENGTH: 117
; FEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (99)...(107)

OTHER INFORMATION: variable
US-09-858-349-2
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US-09-940-727B-13
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Patent No. US20020012909A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SMALL FUNCTIONAL UNITS OF ANTIBODY HEAVY CHAIN VARIABLE REGIONS
FILE REFERENCE: 87534-2800
CURRENT APPLICATION NUMBER: US/09/858,349
CURRENT APPLICATION DOWN: 16

NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3:1
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Publication No. US20030118592A1
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOWAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 30069-401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SSOFTWARE: Patentin version 3.0
LENGTH: 550
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                                                                                                                                                                                                                                                                    Length 266;
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                                                                                                                                                                                                                                                                 Query Match
69.4%; Score 498; DB 15;
Best Local Similarity 79.2%; Pred. No. 2.2e-39;
Matches 95; Conservative 10; Mismatches 15;
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                                                                                                                                                                                OTHER INFORMATION: fusion polypeptide US-10-207-655-260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 79.29
Matches 95; Conservative
NUMBER OF SEQ ID NOS: 426
SOFTWARE: PatentIn version
SEQ ID NO 260
LENGTH: 266
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LENGTH: 136
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US-09-858-349-2
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                                                                                                                                                             FEATURE:
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                                                                                                                                                                                                                                                                    61 NPSLKSRISITRDTSKNKFFLQLNSVTTEDTATYYCVR-----IHYYGYGNWGQGTTL 113
                                                                                                                                                                                                                                               79 NPSLKSRISITRDISKNOFFLOLNSVITGDISTYYCARSLARTIAMDY-----WGQGTSV 133
                                                                                                                                                                                                    1 DVQLQESGPELVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGNRLEWMGYIRYSGITRY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NPSLTSRISISRDTSKNOFFLQLNSVTSEDTATYYCAREWF-PYYFDYWGQGTTLTVSS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DVQLKESGPGLVKPTQTLTLTCTVTGYSITSDYAWNWIRQPPGKGLEWMGYITYSGTTSY
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                                                                                                                                                              19 DVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMGYISYSGITTY
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                                                                                                                      12;
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                                                                                  Length 117;
                                                                                                                      6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: ()..()
OTHER INFORMATION: Synthetic construct of 3B6DIVHv6
                                                                              Score 493; DB 11;
Pred. No. 2.6e-39;
8; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Carr, Francis J.
APPLICANT: Carr, Francis J.
APPLICANT: Hamilton, Anita A.
ITLE OF INVENTION: Carrier molecules
FILE REFERENCE: 229752001700
CURRENT APPLICATION NUMBER: US/10/184,300A
CURRENT APPLICATION NUMBER: PCT/AU02/00827
PRIOR APPLICATION NUMBER: DCT/AU02/00827
PRIOR APPLICATION NUMBER: US 60/301,154
PRIOR APPLICATION NUMBER: US 60/301,154
PRIOR PILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US 60/300,947
NUMBER OF SEQ ID NOS: 12
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 49, Application US/09874141 Publication No. US20330012781A1 GENERAL INFORMATION: APPLICANT: ANDERSON, DARRELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/10184300A; Publication No. US20030124056A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAN, LI-ZHEN
HANNA, NABIL
RASTETTER, WILLIAM H.
KLOETZER, WILLIAM S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial sequence
                                                                              Query Match
Best Local Similarity 78.5%;
Matches 95; Conservative
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Best Local Similarity
Matches 91; Conserv
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-13
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US-09-874-141-49
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APPLICANT:
APPLICANT:
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60 GNKLEYMGYISYSGSTYNPSLKSRISISRDTSKNQFSLKLSSVTAADTGVYYCACRSYG 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MMVLSLLYLLTALPGFLSEVQLQESGPGLVKPSETLSLTCTVSGDSITNGF-WIWIRKPP 59
     COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MRVLILLWLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                               FEATURE:
JOTHER INFORMATION: Description of Artificial Sequence: Synthetic
COTHER INFORMATION: humanized VH#1 amino acid
US-09-874-141-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 11; Length 140;
TITLE OF INVENTION: NON-AGONISTIC ANTIBODIES TO HUMAN GP39, C
TITLE OF INVENTION: CONTAINING, AND THERAPEUTIC USE THEREOF
FILE REFERENCE: 037003-02806.52
CURRENT APPLICATION NUMBER: US/09/874,141
CURRENT FILING DATE: 2001-06-06
NUMBER OF SEQ ID NOS: 53
SOFTWARR: PAUGING DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 53
LENGTH: 140
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Best Local Similarity 71.2%; Pred. No. 1.2e-37;
Matches 99; Conservative 14; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: October 22, 2003, 22:21:46 Job time : 26.428 secs
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                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Artificial Sequence
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October 24, 2003, 03:57:16; Search time 976.125 Seconds (without alignments) 1129.179 Million cell updates/sec
                                                                                                                                                                                                                                              411
1 ATGAGAGTGCTGATTCTTT......CCTCAGTCACCGTCTCCTCA 411
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                   OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. CgnZ 6/ptodata/Z/pubpna/US09B_PUBCOMB.seq;*
CgnZ 6/ptodata/Z/pubpna/US09E_PUBCOMB.seq;*
CgnZ 6/ptodata/Z/pubpna/US09E_MEW_PUB.seq;*
CgnZ 6/ptodata/Z/pubpna/US10A_PUBCOMB.seq;*
CgnZ 6/ptodata/Z/pubpna/US10B_PUBCOMB.seq;*
CgnZ 6/ptodata/Z/pubpna/US10B_NEW_PUB.seq;*
CgnZ 6/ptodata/Z/pubpna/US10B_NEW_PUB.seq;*
CgnZ 6/ptodata/Z/pubpna/US60_NEW_PUB.seq;*
CgnZ 6/ptodata/Z/pubpna/US60_PUBCOMB.seq;*

Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

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6: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

8: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

					SUMMARIES	
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1	281.2	68.4	1420	σ	US-09-237-061-2	Sequence 2, Appli
7	278.6	67.8	363	12	US-10-310-674A-35	Sequence 35, Appl
m	271.4	0.99	806	14	US-10-207-655-259	Sequence 259, App
4	271.4	0.99	1665	14	US-10-207-655-269	Sequence 269, App
S	269	65.5			US-10-184-300A-9	Sequence 9, Appli
9	268	65.2	362		US-10-207-655-257	Sequence 257, App
7	260.8	63.5			US-09-858-349-1	Sequence 1, Appli
ω	259.4	63.1		14	US-10-184-300A-8	Sequence 8, Appli
σ	258.2	62.8	366		US-09-940-727B-101	Sequence 101, App
10	257.8	62.7		14	US-10-184-300A-7	Sequence 7, Appli
11	255.8	62.2		11	US-09-874-141-52	Sequence 52, Appl
12	255.8	62.2		12	US-10-171-681-28	Sequence 28, Appl
13	255.8	62.2		12	US-10-171-680-28	Sequence 28, Appl
14	253.4	61.7		11	US-09-940-727B-105	Sequence 105, App
15	245.6	59.8		11	US-09-940-727B-109	Seguence 109, App
. 16	245.4	59.7		11	US-09-940-727B-113	Sequence 113, App

Sequence 48, Appl Sequence 26, Appl Sequence 43, Appl Sequence 43, Appl Sequence 43, Appl Sequence 27, Appl Sequence 27, Appl Sequence 21, Appl Sequence 34, Appl Sequence 34, Appl Sequence 21, Appl Sequence 27, Appl Sequence 15, Appl
US-09-874-141-48 US-10-171-681-26 US-10-171-681-26 US-10-171-681-26 US-10-174-81-43 US-10-150-762-43 US-10-150-762-43 US-10-150-762-43 US-10-425-529-23 US-10-425-529-24 US-10-425-529-30 US-10-425-529-31 US-10-425-529-31 US-10-425-529-31 US-10-425-529-31 US-10-425-529-31 US-10-330-613-7 US-10-330-613-7 US-10-330-613-7 US-10-330-613-7 US-10-330-613-7 US-10-330-613-7 US-10-330-613-7 US-10-330-613-18 US-10-330-613-18 US-09-925-299-198 US-09-925-299-198 US-09-925-299-198 US-09-925-299-198 US-09-925-299-198 US-09-925-299-198
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ALIGNMENTS

g	1,	. 60	73	120	133	180	193
REGULT 1 US-09-237-061-2 ; Sequence 2, Application US/09237061 ; Sequence 2, Application US/09237061 ; Sequence 2, Application US/09237061 ; Patent No. US20020001624A1 ; GENERAL INFORMATION: APPLICANT: DulPont Pharmaceuticals Company TITLE OF INVENTION: Detection of Patients at Risk for Developing Integrin TITLE OF INVENTION: Antagonist/Agonist Mediated Disease States TITLE OF INVENTION: DASSE CURRENT APPLICATION NUMBER: US/09/237,061 CURRENT FILING DATE: 1998-01-26 PRIOR APPLICATION NUMBER: 60/072,733 PRIOR FILING DATE: 1998-01-27 NUMBER OF SEQ ID NOS: 2 SOFTWARE: PatentIN Ver. 2.0 SEQ ID NO 2 TYPE: DAA ORGANISM: Artificial Sequence FRATURE: OTHER INFORMATION: US/094 US-09-237-061-2	Query Match 68.4%; Score 281.2; DB 9; Length 1420; Best Local Similarity 81.6%; Pred. No. 8e-84; Matches 338; Conservative 0; Mismatches 73; Indels 3; Gaps	Qy 1 ATGAGAGTGCTGATTCTTTTGTGGCTGTTCACAGCCTTTCCTGGTATCCTGTATGTGTG O	Db 14 ATGAAAGTGTTGAGTCTGTTGTACCTGTTGACAGCCATTCCTGGTATCCTGTTGATGTA	Qy 61 CAGCTICAGGAGTCGGGACCTGTCTGGTGAAGCCTTCTCAGTCTCTCTC	Db 74 CAGCTTCAGGAGTCAGGACCTGGCCTCGTGAAACCTTCTCAGTCTCTGTCTCTCACGTCTCTGCCTGC	Qy 121 ACTGTCACTGGCTACTCAATCACCAGTGATCATGCCTGGAGCTGGATCCGGCAGTTTCCA	Db 134 TCTGTCACTGGCTACTCCATCACTGGTTATTACTGGAACTGGATCCGGCAATTTCCA

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GTCTCTGTCCCTCACCTGCACTGTCACTGGCTACTCAATCACCAGTGATCATGCCTGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCAAGATCCCTAGCTCGGACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 TATCACTACCACCCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACACCATCCAA
Sequence 259, Application US/10207655
Publication No. US20030118592A1
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TILE OF INVENTION: BINDING DOMAIN-INMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 39069-401C1
CURRENT APPLICATION NUMBER: US/10/207,655
NUMBER OF SEQ ID NOS: 426
SOFTWARR: Patentin version 3.0
SOFTWARR: Patentin version 3.0
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APPLICANT: Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069,401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT APPLICATION NUMBER: US/10/207,655
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
SEQ ID NO 269
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                                                                                                                                                                                                                                                                                                                                                                                                                          Score 271.4; DB 14; Length 806;
Pred. No. 1.2e-80;
0; Mismatches 61; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42 TGGTATCCTGTCTGATGTGCAGCTTCAGGAGTCGGGACCTGTCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
CRGANISM: Artificial Sequence
FEATURE:
CTHERINGSMATION: fusion polynucleotide
US-10-207-655-269
                                                                                                                                                                                                                                                                                                                                                             ) OTHER INFORMATION: fusion polynucleotide US-10-207-655-259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 269, Application US/10207655; Publication No. US20030118592A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 83.5%;
Matches 308; Conservative C
                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
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US-10-207-655-269
                                                                                                                                                                                                                                                                          LENGTH: 806
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TITLE OF INVENTION: Femily
TITLE OF INVENTION: Femily
FILE REPRENCE: 00140/004001
CURRENT APPLICATION NUMBER: US/10/310,674A
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin version 3.2
SEQ ID NO 35
LENGTH: 363
               240
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67.8%; Score 278.6; DB 12; Length
Best Local Similarity 87.6%; Pred. No. 3.3e-83;
Matches 318; Conservative 0; Mismatches 39; Indels
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US-10-310-674A-35
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 35, Application US/10310674A Publication No. US20030166860A1 GENERAL INFORMATION:
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ORGANISM: Artificial
FEATURE:
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61 ACCTGCACTGTCACTGGCTACTCAATCACAGTGATTATGCCTGGAACTGGATACGGCAG 120
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Publication No. US20030118592A1
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 39069-4011.
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
SEQ ID NO 257
LENGTH: 362
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Pred. No. 1.2e-79;
0; Mismatches 55; Indels
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; Sequence 1, Application US/09858349
; Patent No. US20020012909A1
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Best Local Similarity 84.6%;
Matches 301; Conservative 0
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                                                                                                                                     432 TGGCGGCGGATCTGATGTACAGCTTCAGGAGTCAGGACCTGGCCTCGTGAAACCTTCTCA 491
                                                                                                                                                                             GTCTCTGTCCCTCACCTGCACTGTCACTGCCTACTCAATCACCAGTGATCATGCCTGGAG 161
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                    Length 1665;
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Pred. No. 5.6e-80;
0; Mismatches 45; Indels
                                                          61; Indels
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COTHER INFORMATION: Synthetic construct of 3B6DIVHv7
US-10-184-300A-9
                  271.4; DB 14;
No. 1.7e-80;
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APPLICANT: Carri, Francis J.
TITLE OF INVENTION: Carrier molecules
TITLE REPERENCE: 229752001700
CURRENT FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: US/10/184,300A
CURRENT FILING DATE: 2002-10-26
PRIOR APPLICATION NUMBER: PCT/AU02/00827
PRIOR FILING DATE: 2001-06-26
PRIOR FILING DATE: 2001-06-27
PRIOR FILING DATE: 2001-06-27
PRIOR FILING DATE: 2001-06-27
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.0
SEQ ID NO 9
                                                      0; Mismatches
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Pred.
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Best Local Similarity 86.6%;
Matches 309; Conservative C
                Query Match
Best Local Similarity 83.5%;
Matches 308; Conservative
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US-10-184-300A-9
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                                                                                                                                                                                                                                                                                                                                                            AACCCATCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAGTTCTTC
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                                                                  Score 259.4; DB 14; Length 354; Pred. No. 9.3e-77; 0; Mismatches 51; Indels 3;
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TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE PEFERENCE: 0555/51400-B
CURRENT APPLICATION NUMBER: US/09/940,727B
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 09/214,095
PRIOR APPLICATION NUMBER: PCT/US97/10965
PRIOR APPLICATION NUMBER: PCT/US97/10965
PRIOR FILING DATE: 1996-06-25
PRIOR FILING DATE: 1996-06-25
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.1
  ; OTHER INFORMATION: Synthetic construct of 3B6DIVHv6 US-10-184-300A-8
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Pred. No. 2.4e-76;
0; Mismatches 48;
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Best Local Similarity 84.9%;
Matches 303; Conservative (
                                                                       63.1%;
ilarity 84.9%;
Conservative (
                                                                                               Similarity
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US-09-940-727B-101
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                                                                         Query Match
Best Local Simi:
Matches 303;
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LENGTH: 366
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GENERAL INFORMATION:
APPLICANT: PLAKSIN, Daniel
TITLE OF INVENTION: SNALL FUNCTIONAL UNITS OF ANTIBODY HEAVY CHAIN VARIABLE REGIONS
FILE REFERENCE: 87534-2800
CURRENT APPLICATION NUMBER: US/09/858,349
CURRENT FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
SEQ ID NO.1
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                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: mouse hybridoma specific for H-2D + RGPGRAFVTI peptide
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Pred. No. 3.4e-77;
6; Mismatches 54;
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| Publication No. US20030124056A1
| GENERAL INFORMATION:
| APPLICANT: Carr, Francis J.
| APPLICANT: Hamilton, Anita A.
| TITLE OF INVENTION: Carrier molecules
| FILE REFERENCE: 229752001700
| CURRENT APPLICATION NUMBER: US/10/184,300A
| CURRENT FILING DATE: 2002-10-26
| PRIOR FILING DATE: 2001-06-26
| PRIOR FILING DATE: 2001-06-26
| PRIOR FILING DATE: 2001-06-26
| PRIOR FILING DATE: 2001-06-27
| NUMBER OF SEQ ID NOS: 12
| SOSTWARE: PATENTIN VERSION 3.0
| SEQ ID NO 8
                                                                                                                                                                                                                                                                                                         ; NAME/KEY: misc_feature
; LOCATION: (295)...(320)
; OTHER INFORMATION: a or g or c or t/u
US-09-858-349-1
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 82.3%;
Matches 293; Conservative
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114

Gaps

9

Indels

9

174

234

121 TTTCCAGGAAACAAACTGGAGTGGATGGGCTACATAAGGCACATTTATGGCACTAGGTAC 180

175

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TYPE: DNA ORGANISM: Artificial sequence

NAME/KEY: misc feature LOCATION: ()..()

FEATURE:

235 AACCCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAGTTCTTC 294

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Publication No. US20030012781A1
                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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; NAME/KEY: CDS
; LOCATION: (7)...(426)
US-09-874-141-52
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US-10-171-681-28
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121 CCACCAGGAAAGGGACTGGAGTGGATGGGCTACATAACCTACAGGGGTACCACCATACTAGCTAC 180
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                                                    CTACAGTIGAATICIGIGACIACIGGGGACACGICCACAIAITACIGIGCAAGAICCCIA 354
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                                                                                                                       355 GCTCGGACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 411
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                                                                                                                                               55 GATGTGCAGCTTCAGGAGTCGGGACCTGTCCTGGTGAAGCCTTCTCAGTCTCTGTCCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: ()...(); OTHER INFORMATION: Synthetic construct of 3B6DIVHvS
                                                                                                                                                                                                                             Sequence 7, Application US/10184300A
; Sequence 7, Application US.10184300A
; publication No. US20030124056A1
; GENERAL INFORMATION:
APPLICANT: Carr. Francis J.
APPLICANT: Carrier molecules
TITLE OF INVENTION: Carrier molecules
FILE REFERENCE: 229752001700
; CURRENT FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: US/10/184,300A
; CURRENT FILING DATE: 2002-10-26
; PRIOR FILING DATE: 2001-06-26
; PRIOR FILING DATE: 2001-06-26
; PRIOR FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.0
; FEQ ID NOS: 12
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Best Local Similarity 84.6'
Matches 302; Conservative
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US-10-184-300A-7
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RESULT 11 US-09-874-141-52 ; Sequence 52, Application US/09874141

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GENERAL INFORMATION:
APPLICANT: PAN, LI-ZHEN
APPLICANT: PAN, LI-ZHEN
APPLICANT: PAN, LI-ZHEN
APPLICANT: PAN, LI-ZHEN
APPLICANT: HANNA, NBBLL
APPLICANT: RASTETTER, WILLIAM H.
APPLICANT: KLOETZER, WILLIAM S.
TITLE OF INVENTION: CONTAINING, AND THERAPEUTIC USE THEREOF
FILE REFERENCE: 037003-0280632
CURRENT APPLICATION NUMBER: US/09/874,141
CURRENT APPLICATION NUMBER: US/09/874,141
FILE APPLICATION NUMBER: 06/209,584
PRIOR FILING DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PATENTIN Ver: 2.1
SEQ ID NO 52
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Publication No. US20030170233A1
GENERAL INFORMATION:
APPLICANT: BLACK, Amelia
APPLICANT: PADLAN, Rolardo A.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 62.2%; Score 255.8; DB 11; Best Local Similarity 79.4%; Pred. No. 1.6e-75; Matches 331; Conservative 0; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
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61 CAGCTTCAGGAGTCGGGACCTGTCCTGGTGAAGCCTTCTCAGTCTCTGTCCCTCACCTGC 120
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                                                                        APPLICANT: PADLAN, Eduardo A.
APPLICANT: NEWANN, Roland A.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 CAGCTTCAGGAGTCAGGACCTAGCCTCGTGAACCTTCTCAGACTCTGTCCCTCACCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 12; Length 426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 255.8; DB.12; Length
Pred. No. 1.6e-75;
0; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/171,680
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
APPLICATION NUMBER: US/08/554,840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/332,595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFRENCE/DOCKET NUMBER: 0127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                    COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy 2
COMPUTER: IPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 79.4%;
Matches 331; Conservative
Publication No. US20030175269A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (73) 836-2021
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 426 base pairs
                                       APPLICANT: BLACK, Amelia APPLICANT: HANNA, NAbil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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; LOCATION:
US-10-171-680-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 cagerricadaacteadaaceradeeredaaacerrereadaerereteereereereda 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ACTGTCACTGGCTACTCAATCACCAGTGATCATGCCTGGAGCTGGATCCGGCAGTTTCCA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 rereredededededecreearede -- raargerreregareregareegaaarreeea 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 GGGAATAAACTTGAGTACATGGGCTACATAAGTTACAGTGGTAGCACTTACTACAATCCA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAGTTCTTCCTACAG 300
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                                                                                                                                                            Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 62.2%; Score 255.8; Best Local Similarity 79.4%; Pred. No. 1.6e Matches 331; Conservative 0; Mismatches
                                COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve:
CURRENT APPLICATION UNBER: US/10/171,681
                                                                                                                                                                                                             FILING DATE: 17-UNE-2001
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/925,339
FILING DATE:
APPLICATION NUMBER: US/08/554,840
FILING DATE: 07-NOV-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-127
TELECOMMUNICATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-10-171-680-28
; Sequence 28, Application US/10171680
                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 28: SEQUENCE CHARACTERISTICS:
TENGTH: 426 haracteristics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 426 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                    : Virginia
XY: United States
22313-1404
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Alexandria
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US-10-171-681-28
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Gaps

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183 240

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Search completed: October 24, 2003, 06:22:18
Job time : 977.625 secs
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                                                                                                                                                                                                                                                                                                        TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 ACCTGCACTGTCACTGGCTACTCAATCACGAGGATCATGCCTGGAGCTGGATCCGGCAG 174
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TTGAATTCTGTGACTACTGGGGACACGTCCACATATTACTGTGCAAGATCCCTAGCTCGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACCCATCTCTAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAGTTCTTC 294
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                                                           CTACAGTIGAATICIGIGACTACIGGGACACGICCACATAITACIGIGCAAGAICCCTA 354
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                                                                                                                                 361 ACTACGGC-----TATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL LUNCANALLON.

JELER PARTECULANT: LEANGY, DORAID W
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 0575/51400-8
CURRENT APPLICATION NUMBER: US/09/940,7278
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 09/214,095
PRIOR FILING DATE: 1999-12-28
PRIOR FILING DATE: 1999-7-06-25
PRIOR APPLICATION NUMBER: 09/672,345
PRIOR RILING DATE: 1996-06-25
PRIOR RILING DATE: 1996-06-25
PRIOR RILING DATE: 1996-06-25
PRIOR FILING DATE: 1996-06-25
PRIOR PRILING DATE: 1996-06-25
PRIOR APPLICATION NUMBER: 09/672,345
PRIOR PRILING DATE: 1996-06-25
PRIOR APPLICATION NUMBER: 09/672,345
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TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 0575/51400-B
CURRENT APPLICATION NUMBER: US/09/940,727B
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 09/214,095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
US-09-940-727B-109
; Sequence 109, Application US/09940727B
; Publication No. US20030077793A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                              RESULT 14
US-09-940-727B-105
Sequence 105, Application US/09940727B
Publication No. US20030077793A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: mous
US-09-940-727B-105
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107 GGCTACTCAATCACCCAGTGATTATGCCTGGAACTGGATCCGGCAGTTTCCAGGAACAGA 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 59.8%; Score 245.6; DB 11; Best Local Similarity 87.4%; Pred. No. 4.3e-72; Matches 292; Conservative 0; Mismatches 36;
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PRIOR FILING DATE: 1998-12-28
PRIOR APPLICATION NUMBER: PCT/US97/10965
PRIOR FILING DATE: 1997-06-25
PRIOR APPLICATION NUMBER: 08/672,345
PRIOR FILING DATE: 1996-06-25
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.1
SEQ ID NO 109
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NAME/KEY: misc feature
LOCATION: (56) .. (56)
COTHER INFORMATION: any nucleotide
US-09-940-7278-109
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LOCATION: (49)...(49)
OTHER INFORMATION: any nucleotide
                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: any nucleotide
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NAME/KEY: misc_feature
LOCATION: (28) .. (28)
OTHER INFORMATION: any nucleotide
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OTHER INFORMATION: any nucleotide
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NAME/KEY: misc_feature
LOCATION: (21)...(21)
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TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 411 base pairs
TYPE: nucleic acid
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/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*
                          GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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US-08-757-128-17

US-08-233-16-11

US-08-135-121B-3

US-07-135-399-11

US-09-170-769A-11

US-09-170-769A-11

US-09-170-769A-11

US-09-170-769A-11

US-09-170-769A-11

US-09-170-769A-11

US-09-170-769A-11

US-09-214-095D-105

US-08-252-399-105

US-09-214-095D-105

US-09-214-095D-1135

US-08-138-3011-115

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PCT-US93-08364-88
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Maximum Match 100%
Listing first 45 summaries
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243.4
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Maximum DB &
                                                                                                                                                        OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
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                                                                                                                                                                                                                       Run on:
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3, ,
62,
62,
68,
                                                                                                          Sequence
                              Sequence
Sequence
Sequence
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APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: BALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CUMUNIX:
CUGNIY:
CUGNIY:
CUGNIY:
CUGNITY:
COMPUTER READABLE FORM:
MEDIUM TYPE:
COMPUTER: Floppy disk
MEDIUM TYPE:
COMPUTER:
CO
                      US-08-322-730A-99
US-08-387-874-71
US-08-387-874-71
US-08-397-739-99
US-09-729-597-99
US-08-554-840-26
US-08-925-339-26
US-08-925-339-26
US-08-925-339-26
US-08-925-339-26
US-08-9137-1170-68
                                                                                                                                                                                                                                                                                                                                                                                                        US-08-137-117D-62
US-08-436-717-62
US-09-232-522-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 30, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMAȚION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Foley & Lardner
3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Washington STATE: D.C.
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                                                                                                                                                                   Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 30. Application US/08436717

Patent No. 5817790

GENERAL INFORMATION:

APPLICANT: TSUCHIYA, Masayuki

APPLICANT: BENDIG, Mary

APPLICANT: DONES, Steven

APPLICANT: BENDIG, Mary

APPLICANT: Masayuki

APPLICANT: BENDIG, Mary

APPLICANT: BENDIG, Mary

APPLICANT: Masayuki

TITLE OF INVENTION: NESHAPED HUMAN ANTIBODY TO HUMAN

TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR

NUMBER OF SEQUENCES: 158

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY & Lardner
                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Folgy & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: Washington STATE: D.C. COUNTRY: USA ZIP: 20007-5109 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPPRATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                 Score 411; DB 1; L
Pred. No. 5.6e-132;
                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/08/436,717
                                                                                                                                                                 100.0%;
                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 411; Conservative
                                                                                                 mat_peptide
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                 1..411
                  lineal
               TOPOLOGY:
FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                   ; LOCATION:
US-08-137-117D-30
                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-436-717-30
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                                                                                  FEATURE:
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301 TIGAATICTGIGACTACTGGGGACACGICCACATATTACTGTGCAAGATCCCTAGCTCGG 360
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100.0%; Score 411; DB 1; L
Best Local Similarity 100.0%; Préd. No. 5.6e-132;
Matches 411; Conservative 0; Mismatches 0;
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA: PFB-1992
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
NAME: WEGNER, Harold C.
REGISTRAFION NUMBER: 25,258
REGISTRAFION NUMBER: 25,258
                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17, Application US/08767128
Patent No. 6111079
GENERAL INFORMATION:
APPLICANT: WYLIE, DWANE E.
APPLICANT: LOPEZ, OSVALDO
APPLICANT: MURRAY, PETER JOSEPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           i: 411 base pairs
nucleic acid
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 411 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1..411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-436-717-30
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9 9 120

180

180 240 240 300 360

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APPLICANT: Dornburg, Ralph C.
TITLE OF INVENTION: Cell-Type Specific Gene Transfer Using
TITLE OF INVENTION: Retroviral Vectors Containing Antibody Envelope Fusion
TITLE OF INVENTION: Proteins and Wild-Type Envelope Fusion Proteins
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 ACTGTCACTGGCTACTCAATCACCAGTGATCATGCCTGGAGCTGGATCCGGCAGTTTCCA 180
                                                                        181 AACCCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAGTTCTTC 240
                                                                                                                                                                    241 CTGCAGTTGAATTCTGTGACTACTGAGGACACACACACATATTACTGTGCAAGATGTGGT 300
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                                                                                                                       CTACAGTTGAATTCTGTGACTACTGGGGACACGTCCACATATTACTGTGCAAGATCCCTA 354
                           235 AACCCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAGTTCTTC 294
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                                                                                                                                                                                                                   355 GCTCGGACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 411
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MEDIUM TYPE: Floppy disk

COMPUTER IN FOC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

SOFTWARE: PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/933,616

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US/08/205,980

FILING DATE: 04-MAR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Muccino, Richard R.

REGISTRATION NUMBER: 32,538

REGISTRATION NUMBER: UMD1-025

TELEPHONE: (609) 466-2760

INFORMATION FOR SEQ ID NO:

SEQUENCE CHARACTERISTICS:

LENGTH: 836 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
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69.2%; Score 284.6; DB 2
Best Local Similarity 84.2%; Pred. No. 3.1e-88;
Matches 346; Conservative 0; Mismatches 59
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08933616; Patent No. 5869331; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Richard R. Muccino STREET: P.O. Box 1267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: DNA (genomic)
US-08-933-616-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 836 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Princeton
STATE: New Jersey
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 Accrecacrecacrescracrearcaccasicarrareceregaacregareces
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                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmic
STREET: 3100 No. 6111079west Center, 90 South Seventh St
CITY: Minneapolis
                      LEAD BINDING POLYPEPTIDES AND NUCLEOTIDES CODING THEREFORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.5%; Score 297.8; DB 3
89.6%; Pred. No. 5.6e-93;
iive 0; Mismatches 37
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                                                                                                                                                                                                                                                                                                                                                                                                           US/08/767,128
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 05/00/70/120
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER:
FILING DATE: 04-DEC-1996
CLASSIFICATION TAYA:
APPLICATION NUMBER: PCT/US96/0925
FILING DATE: 05-010N-1996
PRIOR APPLICATION NUMBER: 08/541,373
FILING DATE: 10-0CT-1995
PRIOR APPLICATION NUMBER: 08/462,798
FILING DATE: 05-010N-1995
ATTORNEY/AGENT INFORMATION:
NAME: CATCET, Charles G.
                                                                                                                                                                                                                                  ZIP: 55402
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
SOFFAMER: FastESEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 86.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/371-5278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Coding Sequence
LOCATION: 1...357
OTHER INFORMATION:
US-08-767-128-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: Genomic DNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 357 base pairs
nucleic acid
                                                                          46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 72.5
Best Local Similarity 89.6
Matches 320, Conservative
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APPLICANT: GOEBEL, P
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
                                                                                                                                                                 CITY: Min
STATE: MI
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
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219 240

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Sequence 3, Application US/09135121B

GENERAL INFORMATION:

TITLE OF INVENTION: CELL TYPE SPECIFIC GENE TRANSFER USING RETROVIRAL VECTORS

TITLE OF INVENTION: CONTAINING ANTIBODY-ENVELOPE FUSION PROTEINS AND WILD-TYPE

TITLE OF INVENTION: CONTAINING ANTIBODY-ENVELOPE FUSION PROTEINS AND WILD-TYPE

CURRENT APPLICATION NUMBER: US 08/9135,121B

CURRENT FILING DATE: 1998-08-17

PRIOR PELLING DATE: 1999-08-28

PRIOR APPLICATION NUMBER: US 08/205,980

PRIOR APPLICATION NUMBER: US 08/205,980

PRIOR APPLICATION NUMBER: US 08/205,980

PRIOR APPLICATION NUMBER: US 07/979,619

PRIOR PELLING DATE: 1992-11-20

NUMBER OF SEQ ID NOS: 7

SOFTWARE MICROSOFE WORG 97

SEQ ID NO 3

LENGTH: 836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTCTCAAAAGTCGAATCTCCATCACTCGAGACACATCCAAGAACCAGTACCTGCAG 339
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                                                                                                                                                                                                         163 TCTGTCACTGGCGACTCCATCACCAGTGGTTA---CTGGAACTGGATCCGGAAATTCCCA
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                                                                                                                                                                                                                                                                                               GGAAACAAACTGGAGGGATGGGCTACATAAGTTACAGTGGTATCACTACCAACCCA
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Pred. No. 3.1e-88;
0; Mismatches 59;
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Best Local Similarity 84.2%;
Matches 346; Conservative C
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ORGANISM: Artificial sequence
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US-09-135-121B-3
                                                                                               103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dornburg, Ralph C.
TITLE OF INVENTION: Cell-Type Specific Gene Transfer
TITLE OF INVENTION: Using Retroviral Vectors Containing Antibody-Envelope
TITLE OF INVENTION: Fusion Proteins
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard R. Muccino
STREET: P.O. Box 1267
CITY: Princeton
STATE: New Jersey
163 TCTGTCACTGGCGACTCCATCACCAGTGGTTA---CTGGAACTGGATCCGGAAATTCCCA 219
                                                                                                                                                                                                  TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAGTTCTTCCTACAG 300
                                                                                                                                                                                                                                                                280 reterchanagreganterecenteachedacacatechaganechactacereche 339
                                                                                                                                                                                                                                                                                                                                 TIGAATICTGIGACTACTGGGGACACGTCCACATATTACTGTGCAAGATCCCTAGCTCGG 360
                                                                                                                                                                                                                                                                                                                                                                                                  340 TTGAATTCTGTGACTACTGAGGACACAGCCACATATTACTGTGCAAGAT---ATGGTGGT 396
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                                                                220 GGGAATAAACTIGAGTACATGGGGTACATAAGCTACAGTGGTAGCACTTACTACAATCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                397 AACTATGCTATGGAGTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCA 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 ACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OFTAMING SYSTEM:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/279,307
FILING DATE:
FILING DATE:
CLASSIFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/979,619
FILING DATE:
APPLICATION NUMBER: US/07/979,619
FILING DATE: 20-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: MUCCAINO, RICHARD R.
REGISTRATION NUMBER: 32,538
REFERENCE/DOCKET NUMBER: UMD1-016
TELEPHONE: (609) 466-3407
TELEPHONE: (609) 466-3760
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 036 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , 1e-88;
59;
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Pred. No. 3.1e-
0; Mismatches
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08279307
Patent No. 6146885
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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Best Local Similarity 84.2%;
Matches 346; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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58 GIGCAGCTICAGGAGTCGGGACCIGTCCTGGTGAAGCCTICTCAGTCTCTGTCCCTCACC 117
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                                                                                                                  296 TACAGTIGAATICTGIGACTACTGGGGACACGTCCACATATTACTGTGCAAGATCCCTAG 355
                                                                                                                                                                                                                         608 TGCAGTTGAATTCTGTCACTACTGAGGACACAGCCACATATTACTGTGCAAGA---GGTG 664
236 ACCCATCTCTAAAAGTCGAATCTCTATCACTCGAGACACCATCCAAGAACCAGTTCTTCC
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                                                                                                                                                                                                                                                                                                             665 Gritcecerargerargeacraecegereaaggaaccaeggreaegrereeren 720
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                                                                                                                                                                                                                                                                                                                                                                                                 US-09-065-059-12

| Sequence 12, Application US/09065059 |
| Patent No. 606891 |
| Patent L INFORMATION: |
| APPLICANT: SEINO, Ken-ichiro |
| APPLICANT: YAGITA, Hideo |
| APPLICANT: OKUWURA, Ko |
| APPLICANT: OKUWURA, Ko |
| APPLICANT: NAKATA, MOCOMI |
| TITLE OF INFORTION: THERAPEUTIC AGENT FOR HEPATITIS |
| NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 264.4; DB 3;
Pred. No. 1.8e-81;
0; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 99 Canal Center Plaza CITY: Alexandria STATE: Vire:-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-42,368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 424
ATTORREY/AGENT INFORMATION:
NAME: Bucca Ph.D., Daniel
REGISTRATION NUMBER: P-42,36
REPERENCE/DOCKET NUMBER: 503
REPERENCE/DOCKET NUMBER: 503
RECEGOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64.3%;
84.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              354 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 84.2<sup>3</sup>
Matches 298; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS ADDRESS MCDERMOLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-065-059-12
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                              280 TCTCTCAAAAGTCGAATCTCCATCACTCGAGACACATCCAAGAACCAGTACTACTACTGCAG 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           368 AGGTCAAACTCGAGGAGTCTGGACCTGGCGTGAAACCTTCTCAGTCTCTGTCCCTCA 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 CCTGCACTGTCACTGGCTACTCAATCACCAGTGATCATGCCTGGAGCTGGATCCGGCAGT 175
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TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAGTTCTTCCTACAG 300
                                                                                      TTGAATTCTGTGACTACTGGGGACACGTCCACATATTACTGTGCAAGATCCCTAGCTCGG 360
                                                                                                                              340 TTGAATTCTGTGACTACTGAGGACACCACATATTACTGTGCAAGAT---ATGGTGGT 396
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                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/07956399;
Patent No. 5875717;
GENERAL INFORMATION:
APPLICANT: HAMMURA, TOSHIRO
APPLICANT: HAMMURA, TOSHIRO
APPLICANT: HAMMURA, TOSHIRO
TITLE OF INVENTION: COLYPEPTIDES CAPABLE OF BINDING TO HEAVY
TITLE OF INVENTION: COLYPEPTIDES CAPABLE OF BINDING TO HEAVY
TITLE OF INVENTION: CHAINS OF IL-2 RECEPTORS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                      397 AACTATGCTATGGAGTACTGGGGTCAAGGAACCTCAGTCACGTCTCCTCA 447
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                                                                                                                                                                            361 ACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS_DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/956,399
FILING DATE: 19921005
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5876/17man F.
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: (703) 413-3000
TELEPRAX: (703) 413-220
TELEPRAX: (703) 413-220
TELEPRAX: (703) 413-220
TELEPRAX: GARBSE OPAT UR
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 720 base pairs
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88.2%; Pred. No. 7.4e-86;
ive 0; Mismatches 39
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Best Local Similarity 88.2
Matches 314; Conservative
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US-07-956-399-1
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121 TTTCCAGGAAACAACTGGAGTGGATGGGCTACATAAGGCACATTTATGGCACTAGGTAC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 crecaerredarrereredecrecreadacacecaecararrarrereradararear 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ACCTGCACTGTCACTGGCAATTCAATCACCAGTGATTATGCCTGGACCTGGATCCGGCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTACAGTTGAATTCTGTGACTACTGGGGACACGTCCACATATTACTGTGCAAGATCCCTA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 TACTACGGTTCGGCT-----TACTGGGGCCAAGGGACTCTGGTCACTGTCTCTGCA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 GCTCGGACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 ACCTGCACTGTCACTGGCTACTCAATCACCAGTGATCATGCCTGGAGCTGGATCCGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AACCCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAGTTCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 GATGTGCAGCTTCAGGAGTCGGGACCTGTCCTGGTGAAGCCTTCTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                          CURRENTING SISIEM:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
PEPTICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISCHATION NUMBER: 28,678
REGISCHATION NUMBER: 05.75/51400
TELEPROMONICATION INFORMATION:
TELEPROMUNICATION INFORMATION:
TELEPRAK: 212-278-0400
TELEPRAK: 212-378-0400
                   APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS
CORRESPONDENCE ADDRESS

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51400-A-PCT-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 258.2; DB 2
Pred. No. 2.6e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                   ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 101, Application US/09214095D Patent No. 6280987 GENERAL INFORMATION: APPLICANT: Landry, Donald TITLE OF INVERTION: ANTI-COCAINE CATELE REFERENCE: 51400-A-PCT-US
                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62.8%;
84.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 366 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                  ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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Matches 303; Conserv
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-09-214-095D-101
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US-08-672-345C-87
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1 Application US/09170769A

APPLICANT: LETURCQ, Didier

APPLICANT: MORIATRY, Ann

APPLICANT: MORIATRY, Ann

APPLICANT: TOLEVITCH, Michard

APPLICANT: TOLEVITCH

FILE REFERENCE: SCRIP1140-13

CURRENT FILING DATE: 1998-10-13

FRIOR FILING DATE: 1993-05-28

NUMBER OF SEQ ID NOS: 26

SEQ ID NO 1

SEQ ID NO 1

LEATH: 639
                                                                                                                            181 CCATCTCTCAAAAATCGAATCTCCATCATCGTGACACATCTAAGAACCAGTTTTTCCTG 240
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                               238 CCATCTCTAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAGTTCTTCCTA 297
                                                                                                                                                                                        298 CAGTTGAATTCTGTGACTACTGGGGACACGTCCACATATTACTGTGCAAGATCCCTAGCT 357
                                                                                                                                                                                                                   241 AAGTIGAATICIGIGACIACIGAGGACACAGCCACAIAITACIGIGCGGITIATIACIAC 300
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  191 CTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAGTTCTTCCTGCAGT
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llarity 93.2%; Pred. No. 8.2e-80;
Conservative 0; Mismatches 20; Indels
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Patent No. 5948658
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; LOCATION: (1)..(639)
US-09-170-769A-1
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Best Local Similarity
Matches 272; Conserv
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US-09-170-769A-1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/925,339
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 255.8; DB 3
Pred. No. 1.9e-78;
0; Mismatches 77
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   INFORMATION FOR SEQ ID NO: 28: SEQUENCE CHARACTERISTICS: LENGTH: 426 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 62.2%;
Best Local Similarity 79.4%;
Matches 331; Conservative
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COUNTRY: United States
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STATE: Virginia
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                                                                                                                                                                                                                                                                                               , NAME/KEY:
, LOCATION:
US-08-554-840-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: PADLAN, Eduardo A.
PEPLICANT: NEWMAN, Roland A.
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 355 GCTCGGACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 411
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                                                                                                                                                                                                                                                                                                                                Length 366;
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                                                                                                                                                                                                                                                                                                                         Score 258.2; DB 3;
Pred. No. 2.6e-79;
0; Mismatches 48;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
CITY: Alexandria STATE: Virginia STATE: Virgin
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
NUMBER OF SRQ ID NOS: 121
SSCTWARE: Patentin version 3.0
SEQ ID NO 101
LENGTH: 366
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Sequence 28, Application US/08554840
; Patent No. 6001358
; GENERAL INFORMATION:
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REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 84.9%;
Matches 303; Conservative
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                               TYPE: DNA
ORGANISM: Murine
                                                                                                                                                                                                                                       ; ORGANISM: Muri
US-09-214-095D-101
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GENERAL INFORMATION:
APPLICANT: BLACK, Namelia
APPLICANT: BADLAN, Relia
APPLICANT: PADLAN, Roland A.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
                                                                                                                                                                                         7 AIGAIGGIGITAAGICIICTGIACCIGIIGACAGCCCTICCGGGIIICCIGICAGAGGIG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGAATAAACTTGAGTACATGGGCTACATAAGTTACGGGGAGGTAGCACTTACTACAATCCA
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; Sequence 28, Application Us/09332595
; Patent No. 65063383
; Patent No. 65063383
; Patent No. 650638393
; APPLICANT: BLACK, Amelia
; APPLICANT: BLACK, Amelia
; APPLICANT: BLANNA, Nabil
; APPLICANT: PADLAN, Eduardo A.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN 9p39,
; TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BUTNS, Doane, Swecker & Mathis
sTRREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
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0; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 62.2%; Score 255.8; Best Local Similarity 79.4%; Pred. No. 1.96 Matches 331; Conservative 0; Mismatches
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 07-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTATION NUMBER: 35,030
                                                                                                                                                              TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INPORMATION FOR SEO ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 426 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                REFERENCE/DOCKET NUMBER: 0.
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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US-09-332-595-28
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US-08-672-345C-89
; Sequence 89, Application US/08672345C
; Retent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 255.8; DB 4;
Pred. No. 1.9e-78;
0; Mismatches 77;
                                                                                                                                           FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US/08/554,840
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, RObin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-127
TELECOMMUNICATION:
                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/332,595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.2%;
79.4%;
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TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          . 426 base pairs
nucleic acid
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                                                                                                                             COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATIOS SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/672,345C

FILING DATE: 24-JUN-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REFIRENCE/DOCKET NUMBER: 0575/51400

TELEPHONE: 212-278-0400

TELEPHONE: 212-278-0400

TELEPAX: 212-278-0400

TELEPAX: 212-218-055

INFORMATION FOR SEQ ID NO: 89:

SEQUENCE CHARACTERISTICS:

LENGTH: 366 base pairs
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
COADER ADDRESS:
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 366 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 84.09
Matches 300; Conservative
                                                                                   CITY: New York
STATE: New York
COUNTRY: USA
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Perfect score:

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Minimum Maximum

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BG963370 602083371
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lochar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Prayad by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1636 row: 1 column: 20
High quality sequence stop: 691.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                  BB859416
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                  BB859416
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BI456288
    B1456288 603172678
BU524092 AGENCOURT
BY007948 BY007948
BG962947 602827932
                                                                                                                                     ; Search time 1805.39 Seconds (without alignments) 5532.953 Million cell updates/sec
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1 ATGAGAGTGCTGATTCTTTT......CCTCAGTCACCGTCTCCTCA 411
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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em_gss_ncd...
em_gss_phg...
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342.2 342 329.8 329.4

Score

Ñ. Result

FEATURES

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BY007948 RIKEN full-length enriched, B cells CRL-1702 WEHI 231 cDNA Mus musculus cDNA clone G4D0003J12 5', mRNA sequence.
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Mus musculus
Bukaryota, Matazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Matazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 502)
Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikanido,I., Osato,N., Salto,R., Suzuki,H., Yamanaka,I., Kiyosawa,H.,
Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C.,
Cojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A.,
Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S.,
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                                                                                                                                                                                                                                                                                                                                                                                  /lab host="DHIOB (Tl phage-resistant)"
/clone_lib="NCI_CGAP_CO24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Salj; cloned unidirectionally. Primer: Oligo dT.
Sverage insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 276 c 220 g 229 t
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAW14133 row: d column: 16
High quality sequence stop: 420.
Location/Qualifiers
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Pred. No. 6e-89;
); Mismatches 35;
                                                                                                                                                                                                              1. .963
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
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90.8%;
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Best Local Similarity 90.8
Matches 376; Conservative
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/dev_stage="7 m
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INAGE:6530848 5', mRNA sequence.
BU524092
BU524092.1 GI:22834531
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 CACTGTCACTGGCTACTCAATCACCAGTGATTATGCCTGGAACTGGATCCGGCAGTTTCC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              357 TCGGACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 342.2; DB 12;
Pred. No. 4.5e-89;
0; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166
                                                                  'organism="Mus musculus"
         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 g
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Best Local Similarity 92.3%;
Matches 383; Conservative
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                                          source
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BU524092
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BG962947 6287 659 bp mRNA linear EST 12-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 GGAAACAAAATGGAGTGGATGGGCTACATAAGCTAAAAGTGGTAGCACTAGCTACAACCCA 302
                                                                                                                                                                                                                         183 ACTGTCACTGGCTACTCAATCACCCAGTGATTATGCCTGGAACTGGATCCGGCAGTTTCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                          123 CAGCTTCAGGAGTCGGGACCTGGGCTGAAACCTTCTCAGTTTCTGTCCCTCACCTGC
                                                                                                                                                                    1 ATGAGAGTGCTGATTCTTTTGTGGCTGTTCACAGCCTTTCCTGGTATCCTGATGTG
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                                 Pred. No. 1.6e-85;
0; Mismatches 37; Indels
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Location/Qualifiers
1. .659
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                            89.5%;
                                                                        Matches 368; Conservative
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                            Best Local Similarity
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Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani.

J.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Garbiold, M., Gissi, C., Godzik, A., Godyl, J., Grimmond, S., Gustincioh, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanal, A., Kawali, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Waltais, L., Marchionni, L., McKenzie, L., Miki, P.A., Maglott, D.R., Waltais, L., Marchionni, L., McKenzie, L., Miki, Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, D.U., Reid, J., Ring, B.Z., Rayasi, T., Reed, J.C., Rengie, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, M., Sahadelin, V., Verardo, R., Wayaner, K., Sanadi, J., Mangner, L., Wahastedt, C., Wang, Y., Walls, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Arakawa, T., Konno, H., Nakamura, M., Sakazume, N., Sakazume, N., Shinagawa, A., Yasunishi, A., Yoshinow, W., Imocani, K., Ishibata, K., Shinagawa, A., Yasunishi, A., Yoshinow, M., Materston, R., Lander, E.S., Rogers, J., Blrney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itch,M., Kawai,J., Konno,H., Miyazaki,A., M., Mirata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Matahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suebhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
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//mol_type="mRNA"
//db_xref="taxon:10090"
//clone="400003312"
//cell_type="B_cells"
//cell_line="CRL-1702 WEHI 231"
//clone_lib="RIKEN full-length enriched, B_cells CRL-1702 WEHI 231 CDMA WEHI 231 CDMA
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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MEDLINE PUBMED COMMENT JOURNAL

TITLE

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/ Organism="rub" wilescures
/ mol_type="mRNA"
/ strain="FVB/N"
/ db_xref="taxon:10090"
/ clone="InAGE:4983006"
/ lab_host="DH10B" (T1 phage-resistant)"
/ clone_lib="NCI_CGAP_Co24"
/ note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Not1;
/ note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Not1;
/ note="organ: colon; Vector: pCMV-SPORT6; Site_1: Not1;
/ site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
/ Average insert size 1.6 kb. Constructed by Life
/ Technologies: Note: this is a NCI_CGAP Library."
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 659)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey B. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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80.2%; Score 329.8; DB 13; Length 502;

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BASE COUNT ORIGIN

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Query Match

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120 153 180

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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases I to 483).

Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojina, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, H., Tagawa, Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BB859416 BIKEN full-length enriched, B cells CRL-1702 WEHI 231 CDNA Mus musculus CDNA clone G430007017 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contract: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9226
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
'M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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                                                                                                                          Length
                                                                                                                                                                    45;
                                                                                                                     Score 327; DB 12;
Pred. No. 1.3e-84;
0; Mismatches 45;
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Mus musculus
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88.8%;
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602831999F1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4989229 5',
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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/clone="IMAGE:4989229"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP_Co24"
/note="Grgan: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                       Gaps
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Clone distribution: MGC clone distribution information can letter://image.llnl.gov
http://image.llnl.gov
Plate: LLAMI1003 row. b column: 14
High quality sequence stop: 766.
Llocation/Qualifiers
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                                                                                                       .,
                                                        DB 12; Length 659;
                                                                                                     Indels
                                                                                                       41;
                                                        Score 329.4; DB 1
Pred. No. 2.4e-85;
                                                                                                     0; Mismatches
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/mol_type="mRNA"
/strain="FVB/N"
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                                                        80.1%;
88.7%;
                                                                                                       Conservative
                                                                           Best Local Similarity
Matches 370; Conserv
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/clone lib="NCI_CGAP_Mam5"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sal1;
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sal2;
site 2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov
Plate: LLAM11375 row: m column: 21
High quality sequence stop: 840.
Location/Qualifiers
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 909)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           152 ACTGTCACTGGCTACTCCATCACCAGTGGTTATGCCTGGAACTGGATCCGGCAGTTTCCA
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                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 7.1e-83;
0; Mismatches 48; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
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/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:5151932"
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                                                                                                                               RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno, H., Eukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahára X., Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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602995987F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5151932 5',
mRNA sequence.
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Haysshizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_type="B_cells"
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/clone_lib="RIKEN full-length enriched, B cells CRL-1702
WEHI 231 CDNA"
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Pred. No. 1.3e-83;
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91.3%; Pred. No. 1.5.
1.0 Mismatches '
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/db_xref="taxon:10090"
/clone="G43007017"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information con through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LiAM14018 row: m column: 05
High quality sequence stop: 664.
Location/Oualifiers

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db.care="taxxon:10090"
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/lab_host="DH10B (Ti phage-resistant)"
/clone lih="NCI CGAP Co24"
/note="forgan: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1:6 kb. Constructed by Life
Technologies. Note: this is a NCI CGAP Library."
                                                                                                                               Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases) to 853)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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AGENCOURT 8952317 NCI CGAP_Co24 Mus musculus cDNA clone IMAGE:6477196 5', mRNA sequence.
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Pred. No. 2e-80;
0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
                                                                                                               Mus musculus (house mouse)
                                                                 BQ922384.1 GI:22337415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 76.1%;
Best Local Similarity 93.7%;
Matches 326; Conservative (
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/clone="IMAGE:4224283"
/lab_host="DH10B (TI phage-resistant)"
/clone lib="NUIC CGAP CO24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Sterange insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                           1 (bases 1 to 910)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                           Email: cgapbs-remail.nih.gov
Tissue Procurement: defrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov a column: 20
Plate: LLAMB914 row: a column: 20
High quality sequence stop: 669.
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86.6%; Pred. No. 2.3e-80;
ative 0; Mismatches 54; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                              Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/strain="FVB/N"
                     BF582341.1 GI:11656053
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                                                                                 Mus musculus
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RESULT

BF582341 910 bp mRNA linear EST 12-DEC-2000 602101173F1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4224283 5',

444

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BF578272 933 bp mRNA linear EST 12-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxxn:10090"
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/clone="IMAGB:4207320"
/clone lib="NGI (TI phage-resistant)"
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Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 261 c 245 g 192 t
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: .
http://image.llnl.gov
Plate: LLAM9769 row: o column: 01
High quality sequence stop: 655.
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                        CAGCTTCAGGAGTCGGGACCTGTCCTGGTGAAGCCTTCTCAGTCTCTGTCCCTCACCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGAGAGTGCTGATTCTTTTGTGCTGTTCACAGCCTTTCCTGGTATCCTGTCTGATGTG
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Pred. No. 1.3e-74;
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                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/strain="FVB/N"
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93.7%;
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Best Local Similarity 93.77
Matches 327; Conservative
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DEFINITION
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AUTHORS
TITLE
JOURNAL
                                                                                                                                                                             RESULT 11
                                                                                                                                                                                                                                                                                 ACCESSION
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                    BI249876
602995978F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5151882 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="NCI_CGAP MamS"
/note="Organ: mammary; Vector: pCNV-SPORT6; Site 1: Sall;
Site 2: Notl; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies, Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCAGCTTCAGGAGTCGGGACCTGTCCTGGTGAAGCCTTCTCAGTCTCTGTCCCTCACCTG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CACTGTCACTGGCTACTCAATCACCAGTGATCATGCCTGGAGCTGGATCCGGCAGTTTCC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACTGTCACTGGCTACTCCATCACCAGTACTTATAGCTGGAACTGGATCCGGCAGTTTCC 204
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NIH-WGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84
                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGAGAGTGCTGATTCTTTTGTGGCTGTTCACAGC-CTTTCCTGGTATCCTGATGT
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Plate: LLAM11375 row: k column: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 310.6; DB 1.
Pred. No. 8.7e-80;
0; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue_type="tumor, gross/dev_stage="7 months"
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/clone="IMAGE:5151882"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
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                                                                                                                                      Mus musculus (house mouse)
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                                                                          BI249876
BI249876.1 GI:14797680
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Best Local Similarity 87.2%;
Matches 367; Conservative
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                                                           mRNA sequence.
                                                                                                                                                             musculus
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TITLE
JOURNAL
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KEYWORDS
SOURCE
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BF579775 954 bp mRNA linear EST 12-DEC-2000 602095092F1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4209454 5',
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281 TCTCTCAAAAGTCGAATCTCTGTTACTCGAGACACATCCAAGAACCAGTTCTTCCTGCAG 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/clone="IMAGE:4209454"
/lab_host="DH10B (Tl phage-resistant)"
/clone lib="NUIC CGAP_CG24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1. (bases 1 to 954)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-remail.nih.gov
Tissue produrement: Jeffrey B. Green, M.D.
Tissue produrement: Jeffrey B. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMA775 row: g column: 23
High quality sequence stop: 608.
Location/Qualifiers
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9
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Pred. No. 4.3e-74;
); Mismatches 58; Indels 6;
                                                                              387
                                         TIGAATICIGIGACIACIGGGGACACGICCACAIATIACIGIGCAAG 347
                                                               /organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
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84.6%;
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Matches 352; Conservative
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/Barin="FURBN"
/db_xref="taxon:10090"
/clone="IMAGE:4217294"
/lab_host="PBILOB (Tl phage-resistant)"
/clone=lib="NCI_CGAP_Co24"
/note="Cogan: colon; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP_Library."
                                                                                                                                                                                                   BF580560 866 bp mRNA linear EST 12-DEC-2000 6020903363F1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4217294 5', BF580560
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
Tissue Procurement: Jeffrey E. Green, M.D.
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMM9795 row: n column: 15
High quality sequence stop: 681.
Location/Qualifiers
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MIH-MGC Http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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121 ACTGTCACTGGCTACTCAATCACCAGTGATGATGCCTGGAGCTGGATCCGGCAGTTTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161 ACTGICACTGGCTACTCCATCACCAGTAGTTATAGCTGGAACTGGGTTCGGCAGTTTCCA
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                                                           300 GTTGAATTCTGTGACTACTGGGGACACGTCCACATATTACTGTGCAAGA
                                                                                Indels
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Matches 319; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I. (Dases 1 to 735)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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/strain="FVB/N"
/strain="FVB/N"
/db xxef="taxon:10090"
/clone="InMAGE:14983352"
/lab_host="DH10B (T1 phage-resistant)"
/clone lib="NCI CGAP Co24"
/note="Cogan: colon, Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                    TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAGTTCTTCCTACAG 300
                                                                                              262 TCTCTCAAAAATCGAATCTCCCATCACTGACACATCTAAGAACCAGTTTTCCTGAAG 321
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Tissue Procurement: deffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Colone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
High quality sequence stop: 551.
High quality sequence stop: 551.
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                                                                                                                                                                                           CTGAATTCTGTGACTACTGAGGACACAGCTACATATTACTGTGCAAG
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Mus musculus
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Best Local Similarity
Matches 355; Conserv
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/note="Organ: mammary; Vector: pCWV-SPORT6; Site_l: Sall;
Site_2: NotI; Cloned unidirectionally. Primer: Ōligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
                            TTGAATTCTGTGACTACTGGGGACACGTCCACATATTACTGTGCAAGATCCCTAGCTCGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llni.gov
Plate: LLAM8527 row: h column: 02
High quality.sequence stop: 572.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 741)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                 361 ACTACGGCTA----TGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 411
                                                                                                                                                          372 ACAACGACGACTACTTTGACAACTGGGGCCAAGGCACCACTCTCACAGTCTCCCCA 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to ''.',
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 8.2e-71;
0; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="IMAGE:3488305"
/tissue_type="tumor, gro
/dev_stage="tumor, gro
/lab_host="DH108"
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87.9%;
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Best Local Similarity 87.9
Matches 305; Conservative
                                                                                                                                                                                                                                                                                                                      mRNA sequence.
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KEYWORDS
SOURCE
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AUTHORS
TITLE
JOURNAL
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Humanised antibody
DNA encoding the h
Humanised antibody
Variable heavy sub
Antibody 24-31 hum
Murine wild-type a
DNA encoding the h
scFv(1.1ASML) gene
VH domain of antibod
Monoclonal antibod

DNA encoding 5H7 s Antibody 5H7 heavy Variable region an Variable heavy cha Anti-human FasL an Mouse VH group I(A

Fv(TU27). Homo sa Variable region an Sequence of the an Anti-traseolide 02 Chimeric antibody Variable region an Fv(TU27). Homo sa

Humanised antibody

DNA encoding the h DNA encoding the h Nucleotide sequenc Sequence of PCR pr Anti-VHSV single c

Fusion protein L49 Fd phage clone seq Humanised variable

Sequence of Clone

Antibody 24-31 hu Murine humanised

Run on:

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Human, antibody; interleukin-6; receptor; IL-6R; light chain; L; H;
heavy chain; variable region; mouse; monoclonal; hybridoma; PM1;
plasmid; pPM-k3; pPM-h1; ss.
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                                                                                                                                                                                                                                                                                                                               AAA96550
AAQ30714
AAF76338
AAV99657
AAQ30706
                                                                                        AAA50164
AAA50159
ABZ21160
AAT39555
AAT69539
AAA30416
AAQ80291
AAV09790
ABZ57950
AAT73902
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ABX03771
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AAT62573
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AAT36663
AAV09801
AAV09803
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ABX03769
                                 AAQ40462
ABZ21157
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92JP-0032084
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19-FEB-1992;
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30-MAR-1993
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 Murine 5B3 antibod
Antibody 806 varia
MAD 1.4 heavy chai
Monoclonal antibod
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AntiDNP-scFv. Syn
Anti-dinitrophenol
                                                                              time 204.462 Seconds
alignments)
Million cell updates/sec
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(SIDSI/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*

(SIDSI/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*

(SIDSI/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*

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(SIDSI/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*

(SIDSI/gcgdata/geneseq/geneseqn-embl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
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1 ATGAGAGTGCTGATTCTTT......CCTCAGTCACCGTCTCCTCA
            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                              October 24, 2003, 02:25:30 , Search (without 5426.282
                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                            2552756 seqs, 1349719017 residues
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Maximum Match 100%
Listing first 45 summaries
                                                         - nucleic search, using sw model
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AAT40804
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AAT58258
AAT04584
AAZ51113
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                             N Geneseq 19Jun03;*
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Result

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antibody. It was obtained from total RNA extracted from a SB3 hybridoma by RT-PCR. SB3 is an IgG1 antibody derived from a TNP-KLH immunised mouse. Its binding to TNP or DNS antigen can be blocked by very low amounts of TNT and it can therefore be used in a method for detecting small assayed explosive molecules. Molecules are detected using a plezcelectric sensor. Plezcelectric immunosasaying in liquid phase allows stationary and flow analysis of an aqueous sample. The method is sufficiently sensitive for detection of low molecular weight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATGAGAGTGCTGATTCTTTTGTGGCTGTTCAACCCTTTCCTGGTATCCTGTCTGATGTG
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                               /partial
/product= "5B3 antibody heavy chain variable region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               present sequence encodes the heavy chain variable region of 583
                                                                                                                                                                                                                                                                                                                                                                   Apparatus for detecting small molecules, especially explosives comprises a piezoelectric crystal -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 408 BP; 90 A; 108 C; 99 G; 111 T; 0 other;
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Pred. No. 3e-91;
), Mismatches 35;
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                                                                                                                                                            25-JAN-2000; 2000WO-IL00048.
            /*tag=
                                                                                                                                                                                                                                                                                    Willner I, Eshhar 2;
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                                                                                                                                                                                                                                               The sequences given in AAQ30755-56 were used in example to illustrate the production of a human antibody which recognises human interleukin-6 receptor (LI-6R). The antibody comprises light (L) chain and heavy (H) chain variable regions which were derived from a mouse monoclonal antibody produced from the hybridoma PMI which (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTCTCAAAAAGTCGAATCTCTATCACTCGAGACACACCAGGAACAGTTCTTCCTACAG
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                                                                                                                                    Reconstituted human antibody to human interleukin-6 receptor has low antigenicity and contains mouse V-region complementarity determining regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; 5B3 antibody; IgG1; piezoelectric immunoassay; molecule explosive detection; 2,4,6-trinitrotoluene; TNT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA
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                                                                                                                                                                                                                                                                                                                                                                                           Seguence 411 BP; 95 A; 114 C; 92 G; 110 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 411; DB 13;
; Pred. No. 2.7e-119;
0; Mismatches 0;
                                                     Sato K,
                                                                                                                                                                                                            Disclosure, Page 122-123; 207pp; Japanese.
                                                     Saldanha JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA74604 standard; cDNA; 408 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%;
Matches 411; Conservative 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                  츳
                  CHUS ) CHUGAI SEIYAKU
                                                   Jones ST,
                                                                                      WPI; 1992-398882/48
                                                                                                       P-PSDB; AAR28671
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                                                     Bendig MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated specific binding member (I) which recognizes an epidermal growth factor receptor (EGFR) epitope which is recognizes an epidermal growth factor receptor (EGFR) epitope which is count in tumourigenic. hyperproliferative or abnormal cells and not detectable in normal cells. The EGFR epitope is located within the region comprising residues 273-501 of EGFR and does not demonstrate any amino comprising residues 273-501 of EGFR and does not demonstrate any amino caid sequence alterations or substitutions from normal EGFR. (I) is capable of binding the de2-7 EGFR at an epitope distinct from the capable of binding the de2-7 EGFR at an epitope distinct from the capable of binding the de2-7 EGFR at an epitope distinct from the command wild-type gene. The binding member comprises the VH and VL collypeptide sequence of monoclonal antibody (mAb) 806. (I) is useful for treating or diagnosing human or animal body, especially for treating or treating caneer which is located in or adjacent the communitied EGFR, de2-7EGFR or EGFR with high mannose glycosylation; where EGFR is measured by contacting a biological sample from a mammal in which EGFR to the antibody to occur, and detecting whether binding has occurred between the EGFR from the sample and the antibody, where the detection of binding indicates that presence or activity of the EGFR in eaction of binding indicates that presence or activity of the EGFR in eactivity of an EGFR which indicates the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epidermal growth factor receptor epitope found only in tumorigenic cells, useful for diagnosing, preventing and treating cancer in mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  specific binding members, particularly antibodies recognizing
                                                                                                                   Epidermal growth factor receptor; EGFR; tumourigenic; cytostatic; monoclonal antibody; mAb 806; antibody therapy; tumour; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ritter G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Old LJ, Johns TG, Panousis C, Scott AM, Renner C, Ritte:
Jungbluth A, Stockert E, Collins P, Cavenee WK, Huang H;
Burgess AW, Nice EC;
                                                                                           Antibody 806 variable heavy chain (VH) region encoding DNA.
                                                                                                                                                                                                                            1..54
/*tag= b
55..402
/*tag= c
/note= "806 VH region"
                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 40; Fig 14A; 123pp; English.
             BP.
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            ABZ23940 standard; DNA; 402
                                                                                                                                                                                                                                                                                                                                                              13-MAY-2002; 2002WO-US15185.
                                                                                                                                                                                                                                                                                                                                                                                         11-MAY-2001; 2001US-290410P.
                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-129282/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; ABB82796
                                                                                                                                                                                                                                                                                                          WO200292771-A2
                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Burgess AW,
                                                                 18-MAR-2003
                                                                                                                                                                                                                                                                                                                                     21-NOV-2002
                                                                                                                                                                                                                            sig_peptide
                                                                                                                                                                                                                                                        mat_peptide
                                      ABZ23940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel
ABZ23940
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existence of a tumour or cancer in the mammal. A pharmaceutical composition comprising (I), and optionally vehicle, carrier or diluent is useful for preventing and/or treating cancer in mammals, especially for treating brain-resident cancers that produce aberrantly expressed EGFR in mammals, such as glioblastoma, medulloblastoma, meningioma, neoplastic astrocytoma or neoplastic arteriovenous malformations, and malignant neural tumours in mammals. The present sequence represents the mAb 806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGAATTCTGTGACTACTGGGGACACGTCCACATATTACTGCAAGATCCCTAGCTCGG 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25; Length 402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1..408
/*tag= a
/product= Monoclonal antibody heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 402 BP; 91 A; 102 C; 97 G; 112 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 316.8; DB 2
Pred. No. 1.3e-89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 ACTACGGCTATGGACTACTGGGGTCAAGGAAC 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77.1%;
88.0%;
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Best Local Similarity 88.0
Matches 345; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         VH region encoding DNA.
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WPI; 1998-076914/07.
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                                                  Unidentified
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                                                                                                                                                                           31-DEC-1997
                                                                                                                                                                                                                                                                                          Hayashi K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CAGCTTCAGGAATCGGGACCTGGCGTGAAACCTTCTCAATCTCTGTCCCTCACCTGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 ACTGTCACTGGCTACTCAATCACCAGTGATCATGCCTGGAGCTGGATCCGGCAGTTTCCA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAGTTCTTCCTACAG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGAGAGTGCTGATTCTTTTGTGGCTGTTCACAGCCTTTCCTGGTTTCCTGTCTGATGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGAAACAAACTGGAGCGGATGGGATACATAAGGTACAGTGGTTACACTAGCTACAACCCA
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                       Monoclonal antibodies which inhibit type II phospholipase A2 are useful in the treatment of myocardial infarction, cerebral infarction, acute kidney failure, chronic rheumatism, cardiac shock, pancreatitis, adult respiratory distress syndrome and colitis. The antibodies were generated by immunising Balb/C mice with recombinant human type II phospholipase A2. Spleen cells from the mice were fused with mouse myeloma P3U1 (P3x63Ag8.U1) and the hybridomas obtained were screened for phospholipase A2 inhibitory activity. Active clones were isolated including 12H5, 1.4 and 10.1. These were cultured and the antibody isolated from the culture
                                                                                                                                                                                                                                                                                                     supernatant by precipitation with ammonium sulphate and purification on a column of protein A-Sepharose CL4B. Because the antibody acts on the primate and mouse forms of enzyme as well as human it is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Monoclonal antibody 1.4 heavy chain against type II phospholipase A2
                                                                                                              Monoclonal antibody inhibiting type II phospholipase A2 activity for treatment of myocardial and cerebral infarction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               408
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                                                                                                                                                                                                                                                                                                                                                                                              DB 17; Length 408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 ACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            358 GCCTGCTACTTCGATGTTTGGGGCGCAGGGACAACGGTCACCGTCTCCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATGAGAGTGCTGATTCTTTTGTGGCTGTTCACAGCCTTTCCTGGTATC
                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                     Sequence 408 BP; 96 A; 108 C; 95 G; 109 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                            Query Match 76.3%; Score 313.4; DB 17; Best Local Similarity 86.9%; Pred. No. 1.5e-88; Matches 357; Conservative 0; Mismatches 51;
                                                  Ĥ
                                                  Yasunaga
                                                                                                                                                                                                                                                                                                                                            particularly suitable for preclinical testing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВР
                                                                                                                                                  Example 6; Figure 11; 69pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV12261 standard; cDNA to mRNA; 408
                                                  Takasaki J,
                         (YAMA ) YAMANOUCHI PHARM CO LTD
94JP-0340006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                  Masuho
                                                                         WPI; 1996-333946/33
                                                                                     P-PSDB; AAW01144
29-DEC-1994;
                                                  Kawauchi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-JUN-1998
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The present sequence encodes the monoclonal antibody 1.4 heavy chain against type II phospholipase A2, from the present invention. The present invention describes a novel method for the amelioration of kidney disorders (such as acute renal failure) associated with the administration of cisplatin for the treatment of cancer. The method comprises treatment with a monoclonal antibody which inhibits the cativity of type II phospholipase A2 (particularly of type II phospholipase A2 (particularly of type II phospholipase A2 (particularly of type II phospholipase A2 and contening a part of the possessing the same inhibitory activity and contening a part of the antibody sequence. Preferably the antibody also inhibits the activity of ape and/or mouse type II phospholipase A2, and has the ability to release type II phospholipase A2 bound to a cell membrane. Three specific monoclonal antibodies having these properties which can be used are 12H5, 10.1 and 1.4, derived from hybridomas FERM BP-5300, FERM BP-5298 and FERM BP-5297 respectively. The method can be used for suppressing the nephrotoxicity which is a characteristic feature of cisplatin administration, and therefore allowing more efficient use of this drug as an anticancer agent, e.g. by allowing an increased dosage
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Monoclonal antibody; type II phospholipase A2; inhibition; cisplatin; amelioration; kidney disorder; nephrotoxicity; anticancer; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amelioration of kidney disorders caused by cisplatin administration - by treatment with an antibody inhibiting type II phospholipase A2 activity
                                                                                                                                                                                                                                                                      /*tag= a
/product= "monoclonal antibody 1.4 heavy chain"
/note= "no stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 408 BP; 96 A; 108 C; 95 G; 109 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Takasaki J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 36-37; 74pp; Japanese
                                                                                                                                                                                         cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Masuho Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (YAMA ) YAMANOUCHI PHARM CO LTD
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Best Local Similarity 86.9
Matches 357; Conservative
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TTGACTTCTGTGACTACTGGGACACAGCCACATATTACTGTACAGAGAGACTTGG---AC 357
                                             TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAGTTCTTCCTACAG 300
                                                                                                      TIGAATICIGIGACIACIGGGACACGICCACAIAITACIGIGCAAGAICCCIAGCICGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes the heavy chain variable region for monoclonal antibody (MAD) 13D10, which immunoreacts with a lead cation. The sequence was derived from RNA isolated from hydridoma cells from mouse spleen cells. The protein can be used for binding heavy metals, such as lead cations. It can be used for detecting, removing, adding or neutralising the heavy metals in biological and inanimate systems. It can be used in e.g. aqueous liquid systems, in biological or environmental systems or in such compositions as perfumes, cosmetics, pharmaceuticals, health care products, skin treatment products, pesticides, herbicides, solvents used in the production of semi-conductor and integrated circuit components and production materials
                                                                                                                                                                                                                                                                                                                                                                                   Monoclonal antibody; Fd fragment, lead cation; perfume; cosmetic; pharmaceutical; health care; skin treatment; pesticide; herbicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding heavy metal binding polypeptide sequences - used for detecting, removing, adding or neutralising heavy metals, such as
                                                                                                                                                                411
                                                                                                                                                                                                                                                                                                                                                         Lead binding MAb 13D10 heavy chain variable region encoding cDNA.
                                                                                                                                                                               GCCTGGTACTTCGATGTTTGGGGCGCAGGGACAACGGTCACCGTCTCTCA 408
                                                                                                                                                              ACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA
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/note= "no stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                   BP.
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                                                                                                                                                                                                                                                                   AAT58258 standard; cDNA; 357
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                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murray PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-043140/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                   neavy metal; ss
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Sequence 357 BP; 91 A; 100 C; 79 G; 87 T; 0 other;

for electronic components.

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                                                                                                                                       ACCTGCACTGTCACTGGCTACTCAATCACCAGTGATTATGCCTGGAACTGGATCCGGCAG 120
                                                                                                                                                                                  234
                                                                                                                      115 ACCTGCACTGTCACTGGCTACTCAATCACCAGTGATCATGCCTGGAGCTGGATCCGGCAG 174
                                                                                                                                                                                                                                                                                                          CTACAGTTGAATTCTGTGACTACTGGGGACACGTCCACATATTACTGTGCAAGATCCCTA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The anti-hapten dinitrophenol single chain antibody (anti-DNP scFv) encoded by this sequence is used as a targeting peptide (TP), which is fused to the envelope protein of a retroviral vector. When the TP is fused to the envelope protein, it replaces or disrupts the natural receptor binding site. By using a TP that recognises a cell surface antigen, the retroviral vectors containing TP's can be used in a cell type specific method for introducing genes into cells. These retroviral vectors can be used in the gene therapy of human genetic diseases including, adenosine deaminase (ADA) deficiency, and in clinical trials
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                                                                                                                                                                                                                                                                                                                                                                                                  301 AACTACCCGTGGTACTTTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA 357
                                                                                                                                                                                                         AACCCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACACACAGAAACCAGTTCTTC
                                                                                                                                                                                                                                                                scFv; targeting peptide; retroviral vector; gene therapy;
deaminase deficiency; ADA; cancer; hapten dinitrophenol; ss.
                                                            55 GATGTGCAGCTTCAGGAGTCGGGACCTGTCCTGGTGAAGCCTTCTCAGTCTCTGTCCCTC
                                                                                         GARGIGCAGCITICAGGAGICGGGACCTGGCGTGAAACCITICICAGICTCTGTCCCTC
                                                                                                                                                                                    Gaps
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 357;
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 Length
                              Indels
Score 297.8; DB 18;
Pred. No. 1.2e-83;
0; Mismatches 37;
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 Query Match 72.5%;
Best Local Similarity 89.6%;
Matches 320; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT04584 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti DNP-scFv
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adenosine
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Example, Fig 3, 45pp; English
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21-DEC-1994
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 to cure cancer. A wild type envelope can be used in addition to the altered vector, and will act as a helper molecule. The helper function enhances the infection of cells by the retroviral vector.
                                                                                                                                                                                                       163 TCTGTCACTGGCGACTCCATCACCAGTGGTTA---CTGGAACTGGATCCGGAAATTCCCA
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                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell specific gene transfer using retroviral vectors containing antibody-envelope fusion proteins and wild type envelope proteins
                                                                                                                                                                                                                                                                                                                                                                                     447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Retroviral vector; Spleen Necrosis Virus; SNV; antibody-envelope fusion protein; retroviral envelope protein; gene therapy; antigen binding site; single chain antibody; scPv; dinitrophenol; DNP; cell specific gene transfer; ds.
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                                                              Length 836;
                                                                                                                                                                                                                                                                                                                                                                            361 ACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA
                                                                                                        ATGAGAGTGCTGATTCTTTTGTGGCTGTTCACAGCCTTTCCTGGTATCC
                                                            Score 284.6; DB 16; Length
Pred. No. 2.4e-79;
0; Mismatches 59; Indels
                                        Sequence 836 BP; 219 A; 198 C; 213 G; 206 T; 0 other;
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                                                             Match 69.2%;
Local Similarity 84.2%;
les 346; Conservative (
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The patent discloses a novel retroviral vector, particularly Spleen
Necrosis Virus (SNV) vector, having target cell specificity. The vector
has a targetting envelope which is a chimeric protein consisting of an
antigen binding site of an antibody (e.g. anti-DNP-SCPV) or another
peptide that binds to a specific cell surface protein, fused to the
carboxy terminal part of the retrovial envelope protein. The presence
of the wild type envelope protein serves as a helper molecule to
improve or supplement a functional membrane fusion domain. The
carboxing site replaces the natural viral receptor binding site.
The retroviral vector is used for cell specific gene transfer,
especially in gene therapy. The invention overcomes the restricted host
crange limitation of retroviral vectors. The present sequence is a gene
encoding single chain antibody (serv) against hapten dinturphenol
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Pred. No. 2.4e-79;
0; Mismatches 59; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        targetting envelope of retroviral vector.
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Best Local Similarity 84.2%;
Matches 346; Conservative C
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The present invention describes the detection, in a subject, of antibodies (Ab) that recognise an integrin (1) when bound to its agonist or antigonist (II) comprises forming a (I)-(II) complex, incubating this with source of Ab and detecting Ab that binds.

Crug-dependent antibodies (B) to detect formation of, or increase in, drug-dependent antibodies (DAb) in response to treatment with (II), articlerally to identify treatments less likely to cause side-effects; (b) to identify subjects at increased risk of developing side-effects when treated with (II); (c) to determine if a particular (II) potentiates formation of epitopes recognized by Ab; and (d) to identify (II) less likely to induce DDAb or epitopes recognized by existing DDAb. Chimeric antibodies against a complex of (I) and a particular (II) are used as positive controls in the method. The present sequence represents a specifically claimed chimeric antibody heavy chain nucleotide sequence. (II) are used to treat thromboembolic disorders, e.g. angina pectoris, myocardial infarction, stroke, or pulmonary embolism, but may cause.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGCTTCAGGAGTCAGGACCTGGCCTCGTGAAACCTTCTCAGTCTCTGTCTCTCACCTGC 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      provides a more sensitive detection of DDAb and can be made specific
                                                                                                                                                                                                                                                                                                                                                                                                                   and optimizing treatment of thromboembolic
                                                                                                                                                                                                                                                                                                                                                                                                 Detecting antibodies that recognize complexes of integrin with its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68.4%; Score 281.2; DB 20; Length 1200;
llarity 81.6%; Pred. No. 3.2e-78;
Conservative 0; Mismatches 73; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in some patients.
   thrombocytopenia; thromboembolic disorder; angina pectoris; myocardial infarction; stroke; pulmonary embolism; ss.
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                                                                                                                                                                                                                                                                                                     Dicker IB,
O'Neil KT,
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                                                                                                                                                                                                                                                                                                   Burn TC,
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                                                                                                                                                                                                                                                                                                                       Kochie JE,
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conditions with these modulators
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    responsive antibodies.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 TCTGTCACTGGCGACTCCATCACCAGTGGTTA---CTGGAACTGGATCCGGAAATTCCCA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGATTAAACTTGAGTACATGGGGTACATAAGCTACAGTGGTAGCACTTACTACAATCCA 279
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                                                                                                                                                                                                                                                                                                   The genes coding for the heavy and light chain of an antibody against DNP were provided by Dr Ogawa of Scripps Clinic, La Jolla, Ca. The genes were sequenced and published (Riley et al. 1986). Using PCR a single chain antibody gene was constructed using the signal peptide against DNP. The PCR product was cloned into the Smal site of pBluescript. DNA sequencing confirmed the successful combination of the two gene segments coding for the variable regions of the annigen binding peptide. The complete sequence of the anti-(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                         Retroviral vector with target cell specificity - used for gene therapy by direct injection into a patients bloodstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric; drug dependent antibody; DDAB; integrin; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 68.9%; Score 283; DB 15; Length 836; Best Local Similarity 83.9%; Pred. No. 7.5e-79; Matches 345; Conservative 0; Mismatches 60; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATGAGAGTGCTGATTCTTTTGTGGCTGTTCACAGCCTTTCCTGGTATCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 836 BP; 218 A; 198 C; 213 G; 207 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric antibody heavy chain nucleotide sequence.
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                                                                                                                                                                                                                                                                Example, Fig 3; 23pp; English.
                   93WO-US11258
                                                      92US-0979619
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                                                                                            NEW JERSEY
                                                                                                                                                                  WPI; 1994-200255/24
                                                                                          (UYNE-) UNIV
                                                      20-NOV-1992;
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                                                                                                                               Dornburg RC;
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                                                                                                                                                                GCTCGGACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 AIGIGCAGCTICAGGAGICGGGACCTGTCGGIGAAGCCTTCTCAGTCTCTGTCCCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The constructed plasmids pFv (TU27)-DE and pFv (TU25)-DE which express polypeptides consisting only of the V regions were purified and sequenced. The polypeptides are capable of binding to the beta chain of IL-2 receptor and of inhibiting the binding of IL-2 to the receptor. They are useful as immunomodulators and immunosuppressants, e.g. to prevent graft rejection or to treat inflammatory allergic and autoimmune diseases, or leukemia. Unlike cyclosporin etc. they are both effective and safe. (Updated on 25-MAR-2003 to correct PN field.)
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Pred. No. 1.1e-77;
0; Mismatches 38; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pFv(TU27)-DE; pFv(TU25)-DE; V region; antibody; binding;
heavy; beta; chain; interleukin; II-2; receptor; inhibition;
immunomodulator; immunosuppressant; graft rejection; allergy;
autoimmune disease; leukemia; cyclosporin; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polypeptide(s) which bind H chain of human IL-2 receptors treating inflammatory, allergic and auto-immune disorders, leukaemias etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 720 BP; 186 A; 188 C; 170 G; 176 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; Page 20; 27pp; English.
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88.5%;
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                                                                                                                                                                                                                                                                                                                              AAQ40462 standard; DNA; 720
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(first entry)
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P-PSDB; AAR34510.
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20-AUG-1993
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Matches 315;
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   TCTCTCAAAAATCGAATCTCCATCACTCGTGACACATCTAAGAACCAGTTTTTCCTGAAG 313
                                     TTGAATTCTGTGACTACTGGGGACACGTCCACATATTACTGTGCAAGATCCCTAG---CT 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 ACCTGCACTGTCACTGGCTACTCAATCACGGTGATCATGCCTGGAGCTGGATCCGGCAG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ACCTGCTCTGTCACTGGCTACTCCATCACCAGTGGTTATTACTGGAACTGGATCCGGCAG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene encoding anti-bisphenol A antibody, a recombinant protein and its preparation, a DNA, a vector, a transformant, preparation of a recombinant protein, a kit for determining bisphenol A -
                                                                       314 TTGAATTCTGTGACTACTGAGGACACAGCTACATATTACTGTGCAAGAGATAGAGGGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to sequences for murine heavy chain variable region or light chain variable region of anti-bisphenol A antibody (ABZ21157-ABZ21164 and ABB98905-ABB98912). The sequences are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 GATGTGCAGCTTCAGGAGTCGGGACCTGTCCTGGTGAAGCCTTCTCAGTCTCTGTCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GATGTACAGCTTCAGGAGTCAGGACCTGGCCTCGTGAAACCTTCTCAGTCTCTGTCTCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /partial
/product= "Variable_region anti-bisphenol A antibody
                                                                                                         358 CGGACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 411
374 GACCACGGGGGGTTTGCTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCTGCA 427
                                                                                                                                                                                                                                                                                                                                                                                  anti-bisphenol A; antibody; murine; heavy chain;
                                                                                                                                                                                                                                                                                                                                                 Variable region anti-bisphenol A antibody chain coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
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Pred. No. 4.1e-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "No start or stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful for the preparation of recombinant protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 357 BP; 94 A; 92 C; 79 G; 92 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chain #2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 11; 19pp; Japanese
                                                                                                                                                                                                                                         BP.
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ilarity 86.6%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                         light chain; gene; ds.
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P-PSDB; ABB98906.
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es 309; Conserv
                                                                                                                                                                                                                                                                                                                                                                                      region;
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Pred. No. 4.2e-77;
0; Mismatches 50
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/*tag= d
/label= 5'VH1 primer
340..371
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/label= 3'mVH primer
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/*tag= f
/label= JH01 primer
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10.378
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1.27
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91JP-0294464.
 86.0%;
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(first entry)
            307; Conservative
Best Local Similarity
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11-NOV-1991;
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28-DEC-1992
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                                                                                                                                                 TACAGITGAATTCTGTGACTACTGGGGACACGTCCACATATTACTGTGCAAGATCCCTAG 355
 368 AGGTCAAACTCGAGGAGTCTGGACCTGGCCTGGTGAAACCTTCTCAGTCTCTGTCCCTCA 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to coding sequences for murine heavy chain variable region or light chain variable region of anti-bisphenol A antibody (ABZ21157-ABZ21164 and ABB98905-ABB98912). The sequences are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene encoding anti-bisphenol A antibody, a recombinant protein and its preparation, a DNA, a vector, a transformant, preparation of a recombinant protein, a kit for determining bisphenol A -
                           CCTGCACTGTCACTGGCTACTCACCCAGTGATCATGCCTGGAGCTGGATCCGGCAGT
                                                    cendedecidencedecidecedareacedecidentariocenedeacedecidencedeciden
                                                                               TTCCAGGAAACAAACTGGAGTGGGTTAGGTAGATAAGTTACAGTGGTATCACTACA
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                                                                                                                                                                                                                                        356 CTCGGACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCA 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "Variable region anti-bisphenol A antibody
chain #1"
                                                                                                                                                                                                                                                                                                                                                                                                                    Variable region anti-bisphenol A antibody chain coding sequence #1
                                                                                                                                                                                                                                                                                                                                                                                                                                             Variable region; anti-bisphenol A; antibody; murine; heavy chain;
light chain; gene; ds.
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P-PSDB; ABB98905.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 ACCTGCACTGTCACTGGCTACTCACCAGTGATCATGCCTGGAGCTGGATCGGCAG 174
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                                                                                                       1 GATGTACAGCTTCAGGAGTCAGGACCTGGCCTCGTGAAACCTTCTCAGGTCTCTGTCTCTCT
   Gaps
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                                                             GATGTGCAGCTTCAGGAGTCGGGACCTGTCCTGGTGAAGCCTTCTCAGTCT
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   Indels
203
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completed: October 24, 2003, 03:57:08
ne : 205.462 secs
                                                                                                               10-FEB-1994;
                                                             WO9418330-A1
                                                                                      18-AUG-1994
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                                      Synthetic.
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                                                                                                                                                           antibody-producing hybridoma Wil-a calls. Using this poly(A) RNA as antibody-producing hybridoma UK1-3 calls. Using this poly(A) RNA as a template, an anti-urokinase antibody VK cDNA was amplified with the mC-kappa primer as primer for first strand sysnihesis, and the 3'mV-kappa primer so primers for the PCR. The amplified fragment was restriction disested and ligated into a restriction fragment of pTB1423 to give an anti-urokinase antibody VK cDNA contg. plasmid pTB1456. The sequence of this plasmid is given in AAQ25667. The cDNA is a functional VK gene. The sequence of (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                        Chimeric monoclonal antibodies - contain anti-human fibrin antibody light and heavy chain variable and constant for treating thrombotic conditions e.g. myocardial infarction
                                                                                                                                                                                                                                                                                                                                                          . 9
                                                                                                                                                                                                                                                                                                                              Score 274.6; DB 13; Length 378; Pred. No. 2.5e-76; 0; Mismatches 44; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Binding protein; immobilization; chimeric protein; anchoring protein; Saccharomyces cerevisiae; pUR4143; musk fragrance; traseolide; polymerase chain reaction.
                                                                                                                                                                                                                                                                                                        Sequence 378 BP; 92 A; 100 C; 91 G; 95 T; 0 other;
                                                                                                                                                    Poly(A) + RNA was prepd. from mouse anti-urokinase
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             Tada
                                                                                                                           Example; Figure 15; 87pp; English
             Watanabe T,
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Best Local Similarity 86.4%;
Matches 317; Conservative
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             Taka H,
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27-MAR-1995
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             Iwasa S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Valuable compounds are isolated from complex mixtures by use of immobilized ligands composed of an anchoring protein and a binding protein. A gene encoding such a chimeric protein that will anchor in the cell wall of a lower eukaryote, e.g. S. cerevisiae, and which blinds traseolide with high specificity, was constructed using plasmid pUR4143. This plasmid contains a gene encoding an scPv-TRAS fragment of anti-traseolide antibody 02/01/01 (AAQ67358) obtained by PCR amplification of hybridoma cDNA using primers AAQ67353-54 for the heavy chain, and primers AAQ67355-56 for the light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AACCAACTGGAGTGGATGGGCTACATAAGCTACAGTGGTAGCACTAGCTACCATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immobilised binding proteins for specific cpds - obtd. by expressing chimeric proteins comprising the binding protein and cell wall-anchoring protein in host cells
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PCR; amplification; primer; light chain; hybridoma; scFv; single chain antibody; monoclonal antibody; ds.
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Pred. No. 1.2e-75;
0; Mismatches 37; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Toschka HY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klis FM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 35; 78pp; English
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Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                      93EP-0200350
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                                                                                                                                                                                                                                                                                                                                                                                                             (UNIL ) UNILEVER NV. (UNIL ) UNILEVER PLC.
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October 24, 2003, 02:40:25 ; Search time 1641.41 Seconds (without alignments) 10243.574 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		linear PAT 05-DEC-1998 t., Jones, S. Tarran. and
B ID	6 AR024276 6 AR045129 6 E05314 6 ED011353 6 E05314 6 E05324 6 E05324 6 E05323 10 MUSIGHDQB 10 MUSIGHDQB 11 MUSIGHDQB 12 AX236250 13 MUSIGHDQB 14 MUSIGHDQB 15 MUSIGHDQB 16 AX0276284 17 AX027688 18 MUSIGHAAC 19 MUSIGHAAC 10 MUSIGHAAC 10 MUSIGHAAC 10 MUSIGHAAC 11 MUSIGHAAC 11 MUSIGHAAC 11 MUSIGHAAC 12 MUSIGHAAC 13 MUSIGHAAC 14 MUSIGHAAC 15 MUSIGHAAC 16 MUSIGHAAC 17 MUSIGHAAC 18 MUSIGHAAC 18 MUSIGHAAC 19 MUSIGHAAC 10 MUSIGHAAC 10 MUSIGHAAC 11 MUSIGHAAC 11 MUSIGHAAC 12 MUSIGHAAC 13 MUSIGHAAC 14 MUSIGHAAC 15 MUSIGHAAC 16 MUSIGHAAC 17 MUSIGHAAC 18 MUSIGHAAC 18 MUSIGHAAC 18 MUSIGHAAC 19 MUSIGHAAC 10 MUSIGHAAC 10 MUSIGHAAC 11 MUSIGHAAC 11 MUSIGHAAC 11 MUSIGHAAC 12 MUSIGHAAC 13 MUSIGHAAC 14 MUSIGHAAC 16 MUSIGHAAC 17 MUSIGHAAC 18 MUSIGHAAC 18 MUSIGHAAC 19 MUSIGHAAC 10 MUSIGHAAC 10 MUSIGHAAC 10 MUSIGHAAC 11 MUSIGHAAC 11 MUSIGHAAC 11 MUSIGHAAC 12 MUSIGHAAC 13 MUSIGHAAC 14 MUSIGHAAC 16 AR034254 17 MUSIGHAAC 18 MUSIGHAAC 19 MUSIGHAAC 10 MUSIGHAAC 10 MUSIGHAAC 10 MUSIGHAAC 11 MUSIG	111 bp DNA nt US 5795965. 0 Bendig,M.Margare an interleukin-6 30 18-AUG-1998;
% Query e Match Length DB	1000.0 1000.0	R024276 R024276 R024276.1 GI:397 R024276.1 GI:397 RNOWN. RNOWN. RNOWN. ROBESS I to 411 (bases 1 to 411 Suchiya, M., Sato, aldanha, J. Willian eshaped human to atent: US 5795968
Result No. Score		ARO24276 LOCUS LOCUS DEFINITION SS ACCESSION AN VERSION VERSION VERSION COUNCE UN COUN

240 240 300

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Chimeric antibody against human interleukin-6 receptor.
PI HOSE WILLIAM SALDANHA

PC GOIN33/53, A61K38/00, A61K39/395, A61K39/395, A61F35/00, PC

GOIN33/577/CO7K16/28,

PC CO7K19/00, C12N15/09, (C12N15/09, C12R1:91), A61K37/02, C12N15/00,

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FT mat_peptide (55). (411).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                 301 TIGAATICTGTGACTGCGGGGGGACACGTCCACATATTACTGTGCAAGATCCCTAGCTCGG
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ilarity 100.0%; Pred. No. 4.7e-128;
Conservative 0; Mismatches 0;
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/db_xref="taxon:10095"
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/organism="Mus sp."
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JP 2001083151-A/27
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Reshaped human antibody to human interleukin-6 receptor
Patent: US 5817790-A 30 06-OCT-1998;
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Sequence 30 from patent US 5817790.
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Musculus (house II 
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17-SEP-1993
25-APR-1991 DP 1991095476
TSUCHIYA MASAYUKI, SATO ISAO, MEARII MAAGARETSUTO BENDEITSUGU,
SUTELIBUN TARRN JIYOONZU
C12N15/13//C12P21/08;
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/product='mouse momoclonal antibody H chain
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/organism="Mus musculus"
_---:_ on&"
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/db_xref="taxon:10090"
114 c 92 g 11
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hypothetical: No;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human IL-6 receptor.
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PD 07-SEP-1993
PF 19-FEB-1993
PF 19-FEB-1992 UP 1992032084
PF 19-FEB-1993 UP 1992032084
PC C12N15/06, C12P21/08, C12P21/08, C12Q1/68/C07K15/28, PC C12N15/06, (C12P21/08, C12P21/08, C12Q1/68/C07K15/28, PC C12N15/06, (C12P21/08, C12P21/08, C12P1:91);
PC C12N15/06, (C12P21/08, C12P1:91);
PC C12N15/06, (C12P21/08, C12P1:91);
PC C12N15/06, (C12P21/08, C12P1:91);
PC SCURCE: Clone—PPM-h1;
PF Key
PF Sig_peptide 1. .54
PF Rig_peptide 55. .411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E05354 11 bp RNA linear PAT 29-SEP-1997 DNA encoding V region of H chain of mouse monoclonal antibody against human interleukin-6 receptor.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Tsuchiya, M., Sato,I., Mearii,M.B., Suteilbun,T.J. and Hose,U.S.
RECONSTRUCTED HUMAN ANTIBODY TO HUMAN INTERLEUKIN-6 RECEPTOR
PATENT: JP 1993227970-A 4 07-SEP-1993;
CHUGAI PHARMACEUT CO LTD
                                                                  Gaps
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Best Local Similarity 100.0%; Pred. No. 4.7e-128;
Matches 411; Conservative 0; Mismatches 0;
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/mol type="genomic RNA"
/db_xref="taxon:10095"
_114 c 92 g 11
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mat_peptide 55. .411.
Location/Qualifiers
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JP 1993227970-A/4
07-SEP-1993
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E05354.1 GI:2173543
JP 1993227970-A/4.
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/db xref="caxon:10090"
/cell type="hybridoma"
/cell type="hybridoma"
/codon_start=1
/product="Vh gene product"
/protein_id="CAA29302.1"
/db xref="G1:52827"
/translation="MRVLILCLVAFPGILSDVQLQESGPDLVKPSQSLSLTCTVTG
YSITSGYTWHWINEPEROKIEWMAYIHYSGNTDFNPSLKSRISITRDTSKNOFFLQLN
SVTAEDTATYYCARGYGNYYAMDYWGQGTSVTVSSAKTTPPSVYPLA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MMIGVHR2 450 bp mRNA linear ROD 07-MAY-1992
Mouse mRNA for immunoglobulin heavy chain variable region.
XOS878 Y00330
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Grant. F.J.

Direct Submission

Submitted (31-AUG-1987) Dr. Francis Grant, Zymogenetics, Inc., 2121

North 35th Street, Seattle, Wa 98103, USA

Location/Qualifiers
                                                                                                                                                                                                                                                                                      241 TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACTCCAAGAACCAGTTCTTCCTACAG 300
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 450)
Grant, F.J., Levin, S.D., Gilbert, T. and Kindsvogel, W.
Improved RNA sequencing method to determine immunoglobulin mRNA
                                                                CAGCTTCAGGAGTCGGGACCTGTCCTGGTGAAGCCTTCTCAGTCTCTCTGTCCCTCACCTGC
                                                                                                                                        121 ACTGTCACTGGCTACTCAATCACCAGTGATCATGCCTGGAGCTGGATCCGGCAGTTTCCA
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       1 ATGAGAGTGCTGATTCTTTTGTGGCTGTTCACAGCCTTTCCTGGTATCCTGTCTGATGTG
                                          CAGCTTCAGGAGTCGGGACCTGTCCTGGTGAAGCCTTCTCAGTCTCTGTCCCTCACCTGC
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constant region; Ig heavy chain; variable region
Mus musculus (house mouse)
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/note="constant region (AA 138-149)"
126 c 92 g 116 t
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/note="variable region (AA 1-137)"
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Nucleic Acids Res. 15 (13), 5496 (1987)
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/strain="ML-05"
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Tsuchiya,M., Sato,I., Margaret,B.M., Taren,J.S. and William,S.H.
Tsuchiya,M., Sato,I., Margaret,B.M., Taren,J.S. and William,S.H.
Patent: JP 200116391-A 27 25-APR-2000;
CHUGAI PHARMACEUT CO LTD

Mus Sp. (mouse)

Pu 72 2000116391-A/27

Pu 25-APR-2000
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: C12N15/09,C07K16/18,C07K16/26,C07K19/00,C12N5/10,C12P21/08,
C12N15/00,
                                                                                         GGAAACAAACTGGAGTGGGTACATACATACAGTGGTATCACTACAACCCA
301 TIGAATICIGIGACIACTGGGGACACGICCACAIATIACIGIGAGAGAICCCIAGCICGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                      361 ACTACGCCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 411
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Best Local Similarity
Matches 411; Conserv
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AUTHORS TITLE REFERENCE

RESULT E43823

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/product="immunoglobulin heavy chain"
/protein_id="AAB01613.1"
/do xref="101309342"
/tab.xref=ion="MRVIILL"
/transhahawalRePeOBKLEWMGYITYSGSTSNNPSLKSRISITRDTSKNQFFLQLN
svittbjatxYCARLSVGLRLDYWGQGTTLTVSS"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Pred. No. 2.3e-102;
0; Mismatches 31;
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/db_xref="taxon:10095"
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368. .408
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Matches 377; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukamalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 408)
Iwasaki,Y., Takabatake,H., Shinji,T., Monestier,M. and Ferrone,S.
Structural profile of idiotype, anti-idiotype and
anti-anti-idiotype monoclonal antibodies in the HLA-DQ3 antigenic
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Mus musculus Ig rearranged H-chain mRNA V-region, 5' end of cds
L20961
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Iwasaki,Y., Takabatake,H., Monestier,M. and Ferrone,S.
Idiotypic diversity and variable region gene usage by mouse anti-HLA-DQ3 mAb
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/cell_type="hybridoma"
/tissue_type="hyperimmunized spleen"
/dev_stage="adult"
1. . >408
/standard_name="anti-HLA-DQ3 monoclonal antibody"
/codon_start=1
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           88.8%; Pred. No. 4.9e-103.
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/db_xref="taxon:10090"
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"mol type="mRNA"
'strain="BALB/c"
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           Best Local Similarity 88.8
Matches 365; Conservative
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SVTTEDTATYYCAREAYGYDVGYFDYWGQGTTLTVSSAS"
116 c 99 g 114 t
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monoclonal antibody; processed gene.
Mus musculus (house mouse)
Mus musculus
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Iwasaki,Y. Takabatake,H., Shinji,T., Monestier,M. and Ferrone,S. Structural profile of idiotype, anti-idiotype and anti-anti-idiotype monoclonal antibodies in the HLA-DQ3 antigenic
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Idiotypic diversity and variable region gene usage by mouse
anti-HLA-DQ3 mAb
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                                                                                  Length 423;
                                                                                                                   Indels
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95045941
7957578
                                                                                  Score 332.2; DB 6;
Pred. No. 2.9e-101;
0; Mismatches 33;
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/mol_type="mRNA"
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/sub_species="domesticus"
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/sex="male"
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95331832
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                                                                                    80.8%;
90.6%;
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                                                                                Query Match
Best Local Similarity 90.6
Matches 378; Conservative
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ORGANISM
                                  BASE COUNT
ORIGIN
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VERSION
KEYWORDS
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MUSIGHDOC
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FEATURES
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svTTEDTATYYCARFYDGFDYWGQGTTLTVSS"
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Mus musculus Ig rearranged H-chain mRNA V-region, 5' end of cds.
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Iwasaki, Y., Takabatake, H., Shinji, T., Monestier, M. and Ferrone, S. Structural profile of idiotype, anti-idiotype and anti-anti-idiotype monoclonal antibodies in the HLA-DQ3 antigenic
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/cell_type="hybridoma"
/tissue_type="hyperimmunized spleen"
/dev_stage="adult":
1. . >402
/standard_name="anti-HLA-DQ3 monoclonal antibody"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 ACTACGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCA 411
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/product="immunoglobulin heavy chain"
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95045941
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Pred. No. 1.4e-100;
0; Mismatches 33;
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Best Local Similarity 89.8%;
Matches 369; Conservative
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360. .402
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SVTTEDTATYYCANMITTSAYWYFDVWGAGTTVTVSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 417)
Tempest, P.R.
Direct Submission
Submitted (21-JaN-1994) Philip R. Tempest, ICOS Corporation, 22021
20th Ave SE, Bothell, WA 98021, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAGTTCTTCCTACAG 300
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Tempest, P., White, P., Buttle, M., Carr, F.J. and Harris, W.J. Identification of framework residues required to restore antigen binding during reshaping of a monoclonal antibody against the glycoprotein gB of human cytomegalovirus
Int. J. Biol. Macromol. 17 (1), 37-42 (1995)
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Pred. No. 9e-100;
0; Mismatches 42; Indels 6;
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/mol_type="mww.me.cerus"

/db_xref="taxon:10000"

/db_type="HCMV37"

/cell_type="hybridoma"

/tissue_type="hybridoma"

/closue_type="hyperimmunized spleen"

/closue_type="hyperimmunized spleen"

/closue_lib="Lambda HCMV37"
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Mus musculus
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55. .417
/gene="IgH"
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Matches 369; Conserv
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                                  Iwasaki,Y., Takabatake,H., Monestier,M. and Ferrone,S. Idiotypic diversity and variable region gene usage by mouse anti-HLA-DQ3 mAb manuogenetics 42 (2), 90-100 (1995) 9531832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_"Ype="hybridoma"
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/dev_stage="adult"
1. . >399
/standard_name="anti-HLA-DQ3 monoclonal antibody"
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Pred. No. 2.5e-100;
0; Mismatches 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sub species="domesticus"
db xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                             'organism="Mus musculus"
'mol_type="mRNA"
'strain="BALB/c"
                                                                                                                                                                                                                                                                                               Location/Qualifiers
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Best Local Similarity 94.2%;
Matches 342; Conservative
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        (bases 1 to 399)
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WNGQPAENISWTJSTTTSKTRPKKAPRKAPOKTTVVNDI
SKADPRVOFKTNTSTTTSKTRPKAPTATOFPTENSS
                                                                                                                                                                                                                2 (bases 1 to 1517)
Xao, XW. and Frenkel, M.J.
Direct Submisted (30-JUL-1996) Biomolecular Engineering, CSIRO, 343 Royal
Parade, Parkville, Victoria 3052, Australia
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     284 TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAGTTCTTCCTGCAG 343
                                                                                             Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAAACAAACTGGAGTGGCTGGGCTACATAAACTACAGTGGTAGCACTAGCTACAACAACAA
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Synthetic Mus musculus single chain Fv antibody precursor mRNA,
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Pred. No. 2.1e-97;
); Mismatches 15;
                                                                                                                Mammalia; Eutheria; Rodentia; Sciurogni
1 (bases 1 to 1517)
Xiao, X.W. and Frenkel, M.J.
Full-length immunoglobulin gamma chain
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               341
                                                                                                                                                                                                                                                                                                                                                        'organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:10090"
/cell_line="hybridoma"
                                                                                               Eukaryota; Metazoa; Chordata;
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                                                           Mus musculus (house mouse)
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95.7%;
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Best Local S
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Mus musculus immunoglobulin gamma 1 chain mRNA, complete cds.
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  TCTCTCGAAAGTCGAATCTCTGTCACTCGAGACACATCCAAGAACCAGTTCTTCCTGCAG 300
                                        TTGAATTCTGTGACTACTGGGGACACGTCCACATATTACTGTGCAAGATCCCTAGCTCGG 360
                                                               241 TCTCTCAGAAGTCGAATCTTTTCACTCGAGACACCATCCAAGAACCAGTTCTTCCTGCAG 300
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eshhar, Z. and Willner, I.
Detection of small molecules by use of a piezoelectric sensor
Patent: WO 0433774-A 5 27-JUL-2000;
YISSUM RES DEV CO (IL); ESHHAR ZELIG (IL); WILLNER ITAMAR (IL)
YESUM RES & DEV (IL)
                                                                                                                    361 ACTAC-----GGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 411
                                                                                                                                          TCTGCTTACTGGTATTTCGATGTCTGGGGCGCAGGACCACGGTCACCGTCTCCTCA 417
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8.4e-98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 322;
Pred. No. 8
                                                                                                                                                                                                                                                        AX027688 408 bp
Sequence 5 from Patent WO0043774.
AX027688
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/db_xref="taxon:9606"
108 c 99 g 1:
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Best Local Similarity 90.7%;
Matches 343; Conservative
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Homo sapiens
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Length 1517;

103 120

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223 240

163

283 300

345

complete cds.

RESULT 14

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/ note="recombinant scFv with signal sequence" / codon start=1 / transl_table=11 / transl_table=11 / product="single chain Fv antibody precursor" / protein id="AAB06746.1" / protein id="AAB06746.1" / protein id="MAB06746.1" / translation="MRVLILIWLFAAFPGILSDVQLQESGPGIVKPSQSLSITCTVTG / translation="MRVLILIWLFAAFPGILSDVQLQESGPGSCGSSDFCSCRONSUMTQFPLQLN SVTTSDFTAYCADRSWFAAWQGGTLYVVSAGGSGSGGGGSGSCGSCBOVLMTQFPLSLN VSLGDVSTSCRSGSGSIEHSNGNTYLEWYLOKROGSFGGGGSSCGGGSDVLMTQFPLSLT VSLGDVSTSCRSGSGSIEHSNGNTYLEWYLOKROGSFKLLIYKVSNRFSGYPDFFSGGGGSTPTLKISRVBABDLGVYYCFQGSHVPFFFGAGTKLELKDYKDDDDK"
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                                                                                         Aguinett. Conscision attificial sequences.

I (bases 1 to 825)
Xiao,X.W. and Frenkel,M.J.
Single chain Fv with signal sequence
Unpublished
2 (bases 1 to 825)
Xiao,X.W. and Frenkel,M.J.
Xiao,X.W. and Frenkel,M.J.
Sitoct Submission
Submitted (30-JUL-1996) Biomolecular Engineering, CSIRO, 343 Royal Parade, Parkville, Victoria 3052, Australia
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 CAGCTTCAGGAGTCGGGACCTGGCGGCTGAAACCTTCTCAGTCTGTGTCCCTCACCTGC 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="recombinant mouse light/heavy chain variable
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|db_xref="taxon:10090"
|note="contains Ig heavy chain variable region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. 411
/organism="Mus musculus"
/organism="MRNA"
/db_xref="taxon:10090"
/noTe="contains Ig light chain variable region"
/organism="Mus musculus"
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/product="Ig heavy chain variable region"
793. .816
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/product="single chain Fv antibody"
67. .411
                                                                                                                                                                                                                                                                                                                                                /organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/focus
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Best Local Similarity 95.4%; Pred. No. 6.9e-97;
Matches 329; Conservative 0; Mismatches 16
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/note="linker"
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Search completed: October 24, 2003, 04:50:11 Job time : 1643.91 secs NALA SEL SLANK (uspro)

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October 24, 2003, 02:40:25 ; Search time 1521.59 Seconds (without alignments) 10243.574 Million cell updates/sec
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1 ATGGTGTCCTCAGCTCAGTT.......GGACCAAGCTGGAAATAAAT 381
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GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                     OM nucleic - nucleic search, using sw model
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is the number of results predicted by chance to have a Pred. No.

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	quenq	BD011352 Chimeric	E05353 DNA encodin E43822 Chimeric an	E05419 cDNA sequen	S50261 Ig VL=anti- 133380 Sequence 1	L35316 Mus musculu	M60019 Mouse Ig ka U16689 Mus musculu	AF045496 Mus muscu	AR016717 Sequence	AF466770 Mus muscu	L39092 Mus musculu RC015292 Mus muscu	A51499 Sequence 1	AR085777 Sequence AR024279 Sequence	AR045132 Sequence	BD011356 Chimeric E05357 DNA encodin	E43826 Chimeric an	E05423 cDNA sequen M17160 Mouse Iq ka	AR301133 Sequence	AIOBIBSB MUS MUSCU E06647 CDNA encodi	M27793 Mouse Ig ac	Me0020 Mouse ig Ka BC027418 Mus muscu	AR006747 Sequence	AR038519 Sequence	AR267246 Sequence	S63022 anti-gangli	AR050865 Sequence	AKZ13870 Sequence E07922 cDNA encodi	X55044 M.musculus	X55045 M.musculus X55046 M.musculus	M63611 Mouse Ig re		A linear PAT 05-DEC-1998				et., Jones, S. Tarran. and	receptor
SUMMARIES		AR024275 AR045128	BD011352	E05353 E43822	E05419	\$50261 T33380	MUSIVJR	MUSIGKAAAL MMIII 6689	AF045496	AR016717 MMT05217	AF466770	MUSIGK527A	A51499	AR085777 AR024279	AR045132	BD011356 E05357	E43826	E05423 MUSIGKCKO	AR301133	AY081858 E06647	MUSIGKCPW	MUSIGKAAAM BC027418	AR006747	AR038519	AR267246	S63022	AR050865	AK2198/6 E07922	MMIGKL229	GKL23	1 14	ALIGNMENTS	2	US 5795965.	69		, Bendig, M. Margaret	n. human interleukin-6 5-A 28 18-AUG-1998;
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Chimeric antibody against human interleukin-6 receptor.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.

1 (Dases 1 to 381)
Tsuchiya, M., Sato, K., Bendigu, M.M., Jones, S.T. and Saldanha, H.W.
Chimeric antibody, against human interleukin-6 receptor
Patent: JP 2001083151-A 26 30-MAR-2001;
CHUGAI PHARMACEUTICAL CO LTD
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Best Local Similarity 100.0%; Pred. No. 7.2e-114;
Matches 381; Conservative 0; Mismatches 0; Indels
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mat_peptide (61)..(381).
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JP 2001083151-A/26
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28-JUL-2000 JP 2000229748
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Unclassified.
1 (bases 1 to 381)
Tsuchiya,M., Sato,K., Bendig,M.Margaret., Jones,S.Tarran. and Saldanha,J.William.
Saldanha,J.William.
PReshaped human interleukin-6 receptor Patent: US 5817790-A 28 06-OCT-1998;
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AR045128 GI:5966593
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Tsuchiya,M., Sato,I., Margaret,B.M., Taren,J.S. and William,S.H. Tonchiya,M., 2 antibody against human interleukin-6 receptor Patent: JP 2000116391-A 26 25-APR-2000; CHUGAI PHARMACEUT CO LTD
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JP 2000116391-A/26
25-APR-2000
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JP 2000116391-A/26.
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381 bp RNA linear PAT 29-SEP-1997

DNA encoding V region of L chain of mouse monoclonal antibody

against human interleukin-6 receptor.
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PN JP 1993277970-A/3
PD 07-5EP-1993
PF 19-5EP-1992
PI TSUCHIYA MASAYUKI, SATO ISAO, MEARII MAACARETSUTO BENDEITSUGU,
PI SUTEIIBUN TAREN JIYOONZU, HOSE UIRIAMU SARUDANA PC
CLIANIS/13, CO7KIS/06, CI2NIS/10, CI2P21/08, CI2Q1/68//CO7KIS/28, PC
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                                                                                                                                241 AGGITCAGIGGCAGIGGGICTGGAACAGAITAIICITCICTCACCAITAACAACCIGGAGCAA 300
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 381)
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                                                          GATGGAACTATTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA
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strandedness: Double;
topology: Linear;
*source: clone=pPM-k3;
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/organism="Mus sp."
/wol_type="genomic RNA"
/db_xref="taxon:10095"
a 94 c 84 g 97
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mat_peptide 61. .381.
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JP 1993227970-A/3.
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Best Local Similarity 100.
Matches 381; Conservative
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19 VL-anti-CD4 mAb M-T151 variable region linear ROD 08-MAY-1993 antibody} [mice, hybridoma cells, mRNA Partial, 381 nt]. S50261 G1:260761
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/codon_start=1
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/protein id="AAB4318 1"
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WATYPCQQGNTLPYTFGGGTVKLIYYTSRLHSGVPSRFSGSGSGTDYSLTITNLEQED
3 92 c 83 g 101 t
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Weissenhorn, W., Scheuer, W., Kaluza, B., Schwirzke, M., Reiter, C., Flieger, D., Lenz, H., Weiss, E. H., Rieber, B.P., Riethmuller, G. et, al. Combinatorial functions of two chimeric antibodies directed to human CD4 and one directed to the alpha-chain of the human interleukin-2 receptor 66ee 121 (2), 271-278 (1992)
                                                                                                                                                                                                                        241 AGGTTCAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAACAACCTGGAGCAA 300
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/note="anti-CD4 mAb M-T151 variable region light chain"
61 GATATCCAGATGACACAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACC
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/mol type="mRNA"
/db_xref="taxon:10095"
1. .381
/partial
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MAND MUSCULUS

EUKARYOCT; METAZOA; Chordata; Craniata; Vertebrata; Euteleostomi;
MAND MARGARITA; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Tauchiya, M., Sato, I., Mearii, M.B. and Suteibun, T.J.

DNA CAPABLE OF CODING VARIABLE REGION OF MURINE MONOCLONAL ANTIBODY

TO HUMAN INTERLEUKIN-6 RECEPTOR

AL TO HUMAN INTERLEUKIN-6 RECEPTOR

PATELLI JP 1993216966-A 26 17-SEP-1993;
CHUGAI PHARMACEUT CO LTD

OS (mouse)

PN 17-SEP-1993

PF 25-APR-1991 JP 19911095476

PI TSUCHIYA MASAYUKI SATO ISAO, MEARII MAAGARETSUTO BENDEITSUGU,
PP ST-ARR-1991 JP 1991095476

PT SUTEIIBUN TARRN JIVOONZU

CC STRANGHORS: Double;
CC STRANGHORS: Double;
CC STRANGHORS: NO;
CC ABOUTCE: Cell line=PM1;
CC *BOUTCE: Cell line=PM1;
CC *BOUTCE: Clone=PPM-K3;
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FT MAT_DEPTIGE 1: .60

FT MAT_DEPTIGE FT

CC *BOUTCE: Clone=PPM-K3;
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                                                                                                                                                                                                                                                                                                                                301 GAAGACATTGCCACTTACTTTTTGCCAACAGGGTAACACGCTTCCGTACACGGTTCGGAGGG
  GATGGAACTATTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA
                                                                                                                                   181 GATGGAACTATTAAACTCCTGATCTACTACATCAAGATTACACTCAGGAGTCCCATCA
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Pred. No. 7.2e-114;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA sequence encoding mouse monoclonal antivariable region against human IL-6 receptor.
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Best Local Similarity 100.0%; Pred. No. 7.2
Matches 381; Conservative 0; Mismatches
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Mus musculus (house mouse)
Mus musculus
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MUSIVJR 393 bp mRNA linear ROD 25-WAY-1995
Mus musculus germline immunoglobulin light chain variable region
and joining region mRNA, 5' end.
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/product="immunoglobulin light chain"
/protein id="AAA67439.1"
/db_xref="GI:829183"
/translation="MMSSAOFLGLLLLCFQGTRCDIOMTQTTSSLSASLGDRVTISCR
ASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPSRFSGSGGGTDYSLTISNLEQED
IATYFCQQGNTLPWTFGGGTKLEIKRADA"
                                                                                                                                301 GAAGACATTGCCACTTACTTTGCCAACAGGGTAACACGCTTCCGTACACGTTCGGAGGG 360
181 GATGGAACTGTTAAACTCCTGATCTACACATCAAGATTACACTCAGGAGTCCCATCA 240
                                                                               241 AGGTTCAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAGCAACCTGGAGCAA 300
                                                                                                                                                          301 GAAGATATTGCCACTTACTTTTGCCAACAGGGTAATACGCTTCCGTGGACGTTCGGTGGA 360
                                                         AGGTTCAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAACAACCTGGAGCAA 300
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Mus musculus
Mus musculus
Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Musmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
(bases 1 to 393)
Miller, D.J. and Rodriguez, M.
A monoclonal autoantibody that promotes central nervous system remyelination in a model of multiple sclerosis is a natural
J. Immunol. 154 (5), 2460-2469 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On May 24, 1995 this sequence version replaced gi:529425.
Original source text: Mus musculus (strain SJL/J) hyperimmunized
spleen mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ATGGTGTCCTCAGCTCAGTTCCTTGTCTCTGTTGTTGTTTTCAAGGTACCAGATGT
                                                                                                                                                                                                                                                                                                                                                                                                                        L35316.1 GI:829182
germline; immunoglobulin light chain; joining region; variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db xref="taxon:10090"
/cell_line="SCH94.03"
/cell_type="hybridoma"
/tissue_type="hyperimmunized spleen"
1. .>393 /note="variable region and joining region; putative"
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/function="leader peptide"
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    .393
    /organism="Mus musculus"

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/product="unnamed"
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/strain="SJL/J"
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96 c 8
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Modriguez, M. and Miller, D.J.
Monoclonal antibodies which promote central nervous system remyelination
Patent: US 5591629-A 1 07-JAN-1997;

Location/Qualifiers
1. 339
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                                       Length 381;
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                                     DB 10;
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Pred. No. 1.1e-106;
0; Mismatches 13;
                                     Score 359.2; DB 10
Pred. No. 1.1e-106;
0; Mismatches 13;
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Sequence 1 from patent US 5591629.
133380.1 GI:1824171
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96 c 89 g
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                                       94.3%;
96.6%;
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Best Local Similarity 96.6
Matches 367; Conservative
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/product=1g kappa chain"
/product=1 id="AAA5110".1"
/db_xref="G1:196424".1"
/db_xref="G
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A to mRNA.
Location/Qualifiers
                                                                                                                                                                                                                                                               240
                                                GATATCCAGATGACACCAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACC 120
                                                                                                                                                                                                                                                                                                                                                                   AGGITCAGIGGCAGIGGGICTGGAACAGAITATICTCTCACCATTAACAACCTGGAGCAA 300
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Brigido, M. M. and Stollar, B. D.
Two induced anti-Z-DNA monoclonal antibodies use VH gene segments related to those of anti-DNA aucoantibodies
J. Immunol. 146 (6), 2005-2009 (1991)
1900879
                                                                                 GATATCCAGATGACACAGACTACATCCTCCCTGTCTGCCCTCTCTGGGAGACAGAGTCACC
                                                                                                                                                          ATCAGTTGCAGGGCAAGTCAGGACATTAGCAGTTATTTAAACTGGTATCAGCAGAAACCA
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                                                                                                                                                                                                                                                                                                                181 GATGGAACTGTTAAACTCCTGATCTACTACATCAAGATTACACTCAGGAGTCCCATCA
1 ATGATGTCCTCTGCTCCGTTCCTTGGTCTCCTGTTGCTCTGTTTTCAAGGTACCAGATGT
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M6019
M60019.1 GI:196423
C-region, J-region; immunoglobulin light chain; immunoglobulin-kappa.
Mus musculus
Mus musculus
Rivarian
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/db_xref="Laxon:1000"
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/dev_stage="fetus"
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12. .395
/partial
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72. 395
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Mus musculus Ig light chain leader and variable region Vk V gene family mRNA, partial cds.
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White, K.D., Frank, M.B., Foundling, S. and Waxman, F.J.
Effect of immunoglobulin variable region structure on C3b and C4b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (27-007-1994) Bart Frank, Arthritis and Immunology Program, Oklahoma Medical Research Foundation, 825 NE 13th Street, Oklahoma City, OK 73104, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                   7.1
                                                                                                                                                                                                                                                                                                                                                                                            72 GATTTCCAGATGACGCAGACTACATCCTCCCCTGTCTGCCTCTCTGGGAGACAGAGAGTCACC
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Pred. No. 3.6e-106;
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Mus musculus
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                  72. .356
/gene="IgM"
357. .395
/gene="IgM"
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ATYFCQQGNTLPYTFGGGTKLEIK"
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2 (bases 1 to 378)
Connor.K.C., Farrell, T.P., Morikawa, A. and Stollar, B.D.
Direct Submission
Submitted (02-FEB-1998) Biochemistry, Tufts University School of
Medicine, 136 Harrison Avenue, Boston, MA 02111, USA
1. 378
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AR016717
                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAC04524.1"
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343. .>378
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a 93 c
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58. .342
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                                                                 /codon start=1
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immunīzations"
                                                                                                                                                                                                                                                                                                             /note="encodes R1 through FR3 of immunoglobulin V-kappa"
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                                                                                                                                                                                                                                     61. .381
/product="immunoglobulin light chain variable region"
/note="member of the murine Vk V gene family"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                        Length 381;
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Pred. No. 1.2e-105;
0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                               /note="Jk1 encoded residues"
92 c 83 g 101 t
                                                                                                                                                                                                   1. .60
/note="leader region"
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   sex="female"
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Mus musculus Balb/c anti-platelet integrin gpIIb/IIIa light chain
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J. Immunol. 152 (6), 2968-2976 (1994)
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Mus musculus
Eukaryotalus
Mamalja; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalja; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Direct Submission
Submitted (14-JAN-1994) Man Sung Co, Protein Design Labs., Inc.,
2375 Garcia Ave, Mountain View, CA 94043, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATGGTGTCCTCAGCTCAGTTCCTTGGTCTCCTGTTGCTCTGTTTTCAAGGTACCAGATGT
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                                                                                                                   1 (bases 1 to 381)
Co.M.Sung. and Tso.J.Yun.
Humanized antibodies reactive with GPIIB/IIIA
Patent: US 5777085-A 4 07-JUL-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                   Score 351.2; DB 6;
Pred. No. 4.6e-104;
0; Mismatches 18;
                                                                                                                                                                                                                                                               /organism="unknown"
92 c 83 g
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  GI:3972994
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Best Local Similarity 95.3%;
Matches 362; Conservative (
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U05217.1 GI:460600
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2 (bases 1 to 381)
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Suzuki, K.
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/protein_id="AAA18224.1"
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ASQDINNYLNWYQQKPDGIVKLLIYYTSTLHSGVPSRFSGSGSGTDYSLTISNLEQED
IATYFCQQGNTLPWTFGGGTKLEIK"
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Mus musculus monoclonal antibody BBK-2 light chain mRNA, complete
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/product="anti-platelet integrin gpl1b/IIIa light chain
immunoglobulin".
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Lee,U.H., Kwack,K., Park,J.W. and Kwon,B.S. Direct Submission
Submitted (03.3M-2002) Department of Biological Sciences, University of Ulsan, Ulsan 680-749, Korea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 351.2; DB 10; Length 381; Pred. No. 4.6e-104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     102
organism="Mus musculus'
                                                                   /db_xref="taxon:10090"
/cell_line="C4G1"
                                                                      /cell_line="C4G1"
/cell_type="hybridoma"
/...>381
                                                                                                                                                                                                                                                                                                                                                                                                          /product="unnamed"
92 c 83 g
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                 mol_type="mRNA"
strain="Balb/c"
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95.3%;
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61. .>381
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//ocdon_start=1 / product="monoclonal antibody BBK-2 light chain" / product="monoclonal antibody BBK-2 light chain" / protein id="AAJ76041.1" / protein id="AAJ76041.1" / protein id="AAJ76041.1" / protein id="AAJ76041.1" / protein id="MRFSA0F1.1" / ranslation="MRFSA0F1.1" / rans
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                                                                                                                                                                                                                                    /db_xref="taxon:10090"
41._.745
/note="against human 4-1BB"
                                                                                                 /organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
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Job time : 1526.09 secs
Location/Qualifiers
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ME4 Light Chain V MAb ME4 light chai Coding strand for DNA encoding mouse

p146-k3. Syntheti cDNA encoding ligh Sequence encoding

Sequence encoding
Human IL-1 chimeri
Murine immunoglobu
Rat immunoglobulin
KM641 LA2 immunoglobulin
KM641 H Chain vari
CDNA for humanised
Ganglioside-associ
CDNA for humanised
B-CL11 ymphoma CH
CC19:zeta chimeric

Activating polypep Activating polypep Activating polypep Activating polypep MLV envelope glyco Murine consensus I Chimeric 4H6 anti-Chimeric 4H6 anti-Chimeric 4H6 anti-DNA encoding Immun Murine monoclonal

Murine anti-integr Bispecific CD3-L6F DNA encoding an im DNA encoding recom

Anti-human seminal DNA encoding immun

Title: Perfect score:

Seguence:

OM nucleic

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Run

Scoring table:

Searched:

Database

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Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;
heavy chain; variable region; mouse; monoclonal; hybridoma; PM1;
plasmid; pPM-k3; pPM-h1; ss.
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AAA89088
AAA27323
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ABK13467
AAD01185
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AAQ81076
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AAT73611
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AAQ56067
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AAT73652
ABT14041
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AAA89073
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19-FEB-1992;
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30-MAR-1993
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Anti-CD4 antibody
Mab SCH94.03 light
Mouse C4G1 Ig light
Variable region of
Mouse anti-human F
Mouse anti-human F
MAD VL17E6 light c
                                                                                                     October 24, 2003, 02:25:30 ; Search time 189.538 Seconds (without alignments) 5426.282 Million cell updates/sec
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| SiDSi/gcgdata/geneseq/geneseqn-embl/NA3002.DAT:*
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                                                                                                                                                                                                       1 ATGGTGTCCTCAGCTCAGTT.......GGACCAAGCTGGAAATAAAT 381
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              version 5.1.6
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Maximum Match 100%
Listing first 45 summaries
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AAQ36607
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AAT59500
AAV34426
                                                                            nucleic search, using sw model
                                                                                                                                                                                                                                       IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993
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Query

Score 381

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Result

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                                                                                                                                                                                                                                                                                                              1 ATGGTGTCCTCAGGTCCTTGGTCTCCTGTTGCTTGTTCAAGGTACCAGATGT
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                                                                                   Reconstituted human antibody to human interleukin-6 receptor - has low antigenicity and contains mouse V-region complementarity
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                                                                                                                                                                                                                                                       Query Match 100.0%; Score 381; DB 13; Best Local Similarity 100.0%; Pred. No. 9.1e-109; Matches 381; Conservative 0; Mismatches 0;
                                ×
                                Sato
                                                                                                                          Disclosure; Page 121-122; 207pp; Japanese.
                                Saldanha JW,
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P-PSDB; AAR28670.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 AGGTTCAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAACAACCTGGAGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence encodes the light chain variable region of a preferred anti-CD4 monoclonal antibody for use in the claimed synergistic composition. MAD WT 15.1 is deposited as clone 15-1/p3/14 (ECACC a)0090705). The anti-CD4 antibody is used with at least one anti-IL2R alpha or beta antibody. Individually the antibodies are strongly inhibiting and when used together their immunosuppressive properties are improved; they synergistically inhibit transplant rejection at low doses without significantly reducing the general immune response. See also AAQ36608-Q36616. (Updated on 10-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synergistic antibody compsn. for use as immunosuppressant -comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R alpha- or anti-IL2R beta antibodies
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                                                                                                         /*tag= b
/note= "J2 region begins at position 346"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 381 BP; 105 A; 92 C; 83 G; 101 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scheuer W,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BOEF ) BOEHRINGER MANNHEIM GMBH
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                                                                                                                                                                                                                                                                                                                                                                    91DE-4124759.
91DE-4143214.
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Matches 367; Conservative
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                                                                                                                                                                          GAAGACATTGCCACTTACTTTGCCAACAGGGTAACACGCTTCCGTACACGTTCGGAGGG 360
                                                                                                                                                                                                   301 GAAGATATTGCCACTTACTTTTGCCAACAGGGTAATACGCTTCCGTGGACGTTCGGTGGA 360
                                                                                                                               181 GATGGAACTATTAAACTCCTGATCTACTACATCAAGATTACACTCAGGAGTCCCATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunoglobulin; L-chain; platelet membrane glycoprotein; GPIIa/IIIb; monoclonal antibody; platelet agglutination; humanised antibody; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence encodes the mouse C4G1 immunoglobulin light chain. See AAQ45663 for the heavy-chain coding sequence. The antibody is specific for the GPIIa/IIIb protein and inhibits platelet agglutination. The Ig is thus useful in the treatment of thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contg. immunoglobulin specific for the GP-IIB and -IIIA - for treating disorders related to vascular thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1..63
/*tag= a
/*tag= b
/*tag= b
/note= "C4G1 light chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse C4G1 Ig light-chain coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                           GGGACCAAGCTGGAAATAAA 380
                                                                                                                                                                                                                                                                         361 GCCACCAAGCTGGAAATCAA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PROT-) PROTEIN DESIGN LABS INC. (YAMA ) YAMANOUCHI PHARM CO LTD.
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                                                                                                                                                                                                                                                                                                                                                        AAQ45662 standard; cDNA; 381
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92US-0895952.
92US-0944159.
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(first entry)
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P-PSDB; AAR39265.
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11-SEP-1992;
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29-NOV-1993
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                                                                                                                                                                                                                                                          Monoclonal antibody, MAb; SCH94.03; hybridoma; central nervous system; CNS; demyelination; multiple sclerosis; neural disease; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGGTGTCCTCAGCTCCAGTTCCTTGGTCTCTGTTTTCTAAGGTACCAGATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hybridoma ATCC CRL 11627 was obtd. from a SJL/J mouse injected with spinal cord homogenate from a mammal uninfected with any demyelinating disease. The hybridoma produced a monoclonal antibody (SCH94.03) useful in promoting CNS remyelination. The SCH94.03 light chain germline sequence is given in AAT05311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monoclonal antibodies which stimulate central nervous system re-myelination - are produced by hybridoma ATCC CRL 11627, for treating multiple sclerosis, and viral or post-neural diseases of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 393 BP; 105 A; 96 C; 89 G; 103 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                     GGGACCAAGCTGGAAATAAA 380
                                       GGGACCAAGCTGGAAATAAA 380
                                                                                                                                                                                                                            MAb SCH94.03 light chain DNA.
                                                                                                                                 AAT05311 standard; DNA; 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95WO-US05262.
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                                                                                                                                                                                              02-FEB-1996
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121 ATCAGTTGCAGGGCAAGTCAGGACATTAACAATTATTTAAACTGGTATCAGCAGAAACCA 180
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                                                                                                                                                                                                                         This is the nucleotide sequence of the mouse antibody C4G1 light chain, used in the method of the invention involving the creation of a humanised immunoglobulin (1g) derived from the mouse C4G1 antibody. The humanised Ig capable of binding to GDID/IIIa and inhibiting platelet aggregation and also the releasing reaction of platelets. The Ig can be used for treating cardiovascular diseases and thromboembolic disorders, e.g. acute myocardial infarction, unstable angina, stroke, transient ischemic episodes, deep vein thrombosis and pulmonary embolism, extracorporeal cardiopulmonary circulation. The Ig can also be used in diagnoshing the presence and location of a thrombus, or certain types of cancer cells which develop GPID/IIIa on their surfaces, for the detection of GPID/IIIa antigness or for isolating platelets. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAGATATTGCCACTTACTTTTGCCAACAGGGTAATACGCTTCCGTGGACGTTCGGTGGA 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ATGGTGTCCTCAGCTCCGTTCCTTGGTCTCCTGTTGCTCTGTTTTCAAGGTACCAGATGT
                                                                                                      New humanised immunoglobulin which binds GPIIb/IIIa - derived from mouse C4G1 antibody, used for inhibiting platelet aggregation for treating cardiovascular and thromboembolic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, Fas ligand, antigen, neutral, antibody, apoptosis, HIV, induction, assay, enzyme linked immunosorbant assay, diagnosis, disease, hepatitis B, hepatitis C, human immunodeficiency virus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 19; Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse anti-human Fas ligand antibody F919 light chain cDNA.
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0; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 381 BP; 104 A; 92 C; 83 G; 102 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.2%; Score 351.2;
95.3%; Pred. No. 1.8
                                                                                                                                                                                          Disclosure; Fig 2A; 35pp; English
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hes 362; Conservative
                                           WPI; 1998-398136/34.
                                                                 P-PSDB; AAW49809
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                                                                                                                                                                                                                                                     AGGTTCAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAACAACCTGGAGCAA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse; antibody C4G1; light chain; humanised; immunoglobulin; Ig; inhibition; antigen; cardiovascular disease; thromboembolic disorder; cancer; acute myocardial infarction; unstable angina; stroke; transient ischemic episode; pulmonary embolism; deep vein thrombosis; extracorporeal cardiopulmonary circulation; ss.
                                                                                      Gaps
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0
                                         DB 14; Length 381;
                                                                                    Indels
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  T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Variable region of mouse antibody C4G1 light chain.
                                                                                  18;
                                       92.2%; Score 351.2; DB 1.
llarity 95.3%; Pred. No. 1.8e-99;
Conservative 0; Mismatches 18
Sequence 381 BP; 104 A; 92 C; 83 G; 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGACCAAGCTGGAAATAAA 380
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91US-0812111.
92US-0895952.
92US-0944159.
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YAMANOUCHI PHARM CO
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/product= '
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                                                            Local Similarity
les 362; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-DEC-1991;
09-JUN-1992;
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24-SEP-1998
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                                           Query Match
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This cDNA encodes the light chain of the mouse antibody F919-9-18. This is used for generating a mouse anti-human Fas ligand monoclonal antibody. The invention provides the use of Fas antegonist as an agent for the treatment and prevention of apoptosis-related diseases. The Fas antagonist can be a partial Fas antigen peptide containing the extracellular part of the protein, but lacking the signal sequence, an anti-Fas antibody, or an anti-Fas ligand antibody, where the antibody is preferably a humanised antibody. The Fas antagonist is used in the treatment and prevention of diseases such as myocardial infarction, heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                failure, ischemic heart disease, acute kidney failure, graft-versus-host disease, ischemic restenoais of the heart, liver or kidney, and endotoxic shock, and also as an organ preservative in transplantation. The agent is of low toxicity but effectively inhibits the Fas/Fas ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ATGATGTCCTCTGCTCGAGTTCCTTGGTCTCCTGTTGTTTTCAAGGTACCAGATGT
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                                                                                                                                                                                                                                                                      Fas ligand; Fas antagonist; apoptosis related disease; liver disease;
                                                                                                                                                                                                                                                                                         heart failure; kidney failure; graft-versus-host disease; antibody; myocardial infarction; ischemic restenosis; endotoxic shock; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 19; Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of Fas antagonist for treatment and prevention of apoptosis-related diseases - such as heart or kidney failure,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "F919-9-18 light chain"
/note= "the stop codon is not indicated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 381 BP; 102 A; 94 C; 85 G; 100 T; 0 other;
                                                                                                                                                                                                                           Mouse antibody F919-9-18 light chain encoding cDNA.
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ilarity 95.0%; Pred. No. 5.7e-99;
Conservative 0; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  graft-versus-host disease or liver disease
                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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    361 GGCACCAAGCTGGAAATCAA 380
                                                                                                       ВР
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                                                                                                       AAV34426 standard; cDNA; 381
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nes 361;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibody reactive with Fas ligand capable of inducing apoptosis - used for diagnostic assay of Fas ligand in body fluids and for treatment of diseases in which Fas ligand/Fas antigen is involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anti-apoptosis inducing human Fas ligand, monoclonal antibody, F919. The antibody can be used in a Fas ligand assay, e.g. an enzyme linked immunosorbant assay, to diagnose diseases in which the Fas ligand/Fas antigen system is implicated, e.g. hepatitis B/C, human immunodeficiency virus, graft/host disorders, ulcerative collitis or sequelae of myocardial infarction. The antibody may also be used to treat such diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 18; Length 381;
graft versus host disease; ulcerative colitis; sequelae;
myocardial infarction; mouse; murine; monoclonal; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence encodes the light chain of the mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  Vasquez M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence 381 BP; 102 A; 94 C; 85 G; 100 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91.8%; Score 349.6;
95.0%; Pred. No. 5.7e
ive 0; Mismatches
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                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Nagata S,
                                                                                                                                                                                                                                                                                                                                                                   (MOCH ) MOCHIDA PHARM CO LTD. (OSAB-) OSAKA BIOSCIENCE INST
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                                                                                                                          .381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-108917/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAW11815.
                                                                                                                                                                                   WO9702290-A1
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matrix interactions caused by alphaV integrin; which blocks tumo development and which has no cytotoxic activity, may be used to treat tumours, especially melanoma (but also glioma, carcinoma) optionally coupled to a cytokine such as interleukin-2. The monoclonal antibody may also be used for diagnostic imaging of tumours and assesment of tumour growth when conjugated to a radio opaque-agent.
                                                                                         Sequence 381 BP; 105 A; 88 C; 85 G; 103 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monoclonal antibody, chimera, light, heavy, chain, variable, antigen; diagnosis; cancer; tumour; ss.
                                                                                                                                     19;
                                                                                                             91.5%; Score 348.6; DB 1.95.0%; Pred. No. 1.2e-98; ive 0; Mismatches 19
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88US-0241744.
88US-0243739.
88US-0253002.
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(first entry)
                                                                                                                                     Conservative
                                                                                                                          Best Local Similarity
Matches 360; Conserv
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08-SEP-1988;
13-SEP-1988;
04-OCT-1988;
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04-MAR-1993
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                         GATATCCAGATGACACACACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACC
                                                                       121 ATCAGTTGCAGGGCCAGTCAGGACATTAGCAATTATTAAACTGGTATCAGCAGAAACCA
                                                                                                                  GATGGAACTGTTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA
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                                                                                                     GATGGAACTATTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA
                                                                                                                                                AGGTTCAGTGGCAGTCTGGAACAGATTATTCTCTCACCATTAACAACCTGGAGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A monoclonal antibody which reacts only with the alphav chain of human alphav integrins; which blocks attachment of alphav integrin bearing cells to integrin substrate; which reverses established cell
                                                                                                                                                                                                                                                                                                                                                                                                      Monoclonal antibody; MAb; integrin; cell-matrix interaction;
tumour; melanoma; glioma; carcinoma; cytokine; interleukin-2; IL-2;
imaging; detection; radiolabel; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 14; Figure 17a; 54pp; English.
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/*tag=
61..381
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P-PSDB; AAR99003.
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DB 17; Length 381;
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121 ATCAGTTGCAGGGCAAGTCAGGACATTAGCAGTTATTTAAACTGGTATCAGCAGAAACCA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A cDNA clone (AAT43440) codes for the light chain variable region the way of the oligo-dC tail to the Jkappa jucketong from the oligo-dC tail to the Jkappa jucketion. It was obtd. from an ME4 hybridoma cDNA library by screening with a mouse C kappa region probe. MAD ME4 (IgG1) binds to an antigen that is expressed on the surface of human melanoma and lung, breast, colon and ovary carcinomas, but not on most normal adult tissues. Heavy chain and light chain variable region (see also AAT4334-43) sequences can be used with human constant region sequences to express mouse-human chimeric antibodies in transformed host cells. The antibodies have specificity to human tumour antigens and can be used for human cancer treatment and diagnosis.
                     Chimeric antibody; monoclonal antibody; ME4; antibody engineering; tumour; antigen; breast carcinoma; lung carcinoma; colon carcinoma; ovary carcinoma; melanoma; cancer; diagnosis; therapy; light chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric mouse-human antibodies - recognise a human tumour antigen, used for the treatment and diagnosis of human cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91.3%; Score 348; DB 18; Length 444; 94.7%; Pred. No. 1.9e-98; ive 0; Mismatches 20; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Robinson
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/*tag= a
/product= Me4 light chain V region
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                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Horwitz AH,
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88US-0240624.
88US-0241744.
88US-0253002.
89US-0367641.
89US-036761.
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Best Local Similarity 94.7
Matches 360; Conservative
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04-OCT-1988;
19-JUN-1989;
21-JUL-1989;
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06-SEP-1988;
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                                                                                                                                                                                                                                                                                                                       Shown is the nucleotide sequence from the end of the oligo-dC tail to the Jkl-Ck junction. The sequence is used in the prodn. of a chimeric antibody mol. comprising two light chains and two heavy chains, each having a constant region (human) and variable region (murine) having specificity to an antibodies can be used for any purpose for which the original murine Mabs can be used, with the advantage that they are more compatible with the human body. They are esp. used for the diagnosis and treatment of cancer.

(Updated on 25-MAR-2003 to correct PA field.)
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0
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                                                                                                                   Chang CP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 444 BP; 109 A; 122 C; 94 G; 119 T; 0 other;
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                                                                                                                                                                                                                                                                                     Claim 13; Page 123 + Fig 29; 173pp; English.
                                                                                                                   Lei
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                                                                                                                 Better MD, Horwitz AH, Robinson RR,
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89US-0367641
89US-0382768
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Best Local Similarity 94.7
Matches 360; Conservative
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19-JUN-1989;
21-JUL-1989;
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13-FEB-1997
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antibody-dependent cellular cytotoxicity to target cells. The chimeric antibodies can be used for therapeutic purposes in the treatment of human cancer. (Updated on 20-MAR-2003 to correct PR field.)
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                                                                                                          Query Match
91.3%; Score 348; DB 20; Length 444;
Best Local Similarity 94.7%; Pred. No. 1.9e-98;
Matches 360; Conservative 0; Mismatches 20; Indels 0
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                                                                               Sequence 444 BP; 109 A; 122 C; 94 G; 119 T; 0 other;
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88US-0240624.
88US-0241744.
88US-0243739.
88US-0253002.
89US-0367641.
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27-DEC-1994;
06-SEP-1988;
08-SEP-1988;
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19-JUN-1989;
21-JUL-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence encodes the light chain variable region of murine antibody ME4. The sequence was used to create chimeric mouse-human immunoglobulins which recognise the human tumour antipen bound by antibody IMC1 (produced by hybridoma cell line ATCC HB 9812). The chimeric antibodies also have an antigen-binding site that competitively inhibits the binding of antibody IMG-1, and mediate complement-dependent cytolysis of target cells or
                                                                                                                                                                                                                                                                                                                                                                                                                                      Light chain variable region; murine antibody ME4; antibody ING-1; chimeric immunoglobulin; human tumour antigen; chimeric antibody; treatment; human cancer; 88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/note= "partial CDS, no termination codon"
                                                                                                                                                                                                                                                                                                                                                                                                           strand for mouse ME4 light chain variable region.
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88US-0243739.

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99US-0382768.
                                                                                                                                                                                                                                                                                               AAV71158 standard; DNA; 444
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P-PSDB; AAW85062.
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06-MAY-1991;
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16-APR-1999
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The invention describes an antibody comprising a human constant region and a variable region having specificity for the human tumour antigen bound by the ING-1 antibody, where the ING-1 is produced by cell line (HB9812 as deposited with ATCC, and the antibody has the same affinity as the ING-1 for the human tumour antigen. The antibody is useful in an immunoassay method for detecting an antigen in a sample by contacting a label detectable entigen in the sample with the antibody, detecting the label and relating the detected label to the presence of the antigen; or suspected of containing the antibody with a part of the animal subject of the antigen; and the presence of the antigen in an animal by contacting the antibody with a part of the animal effected label to the presence of the antigen; and for killing cells carrying an antigen by contacting the cells with the antibody and clarying the killing to cocur. The antibodies are useful in tumour diagnosis and therapy. The chimeric antibodies bind to the surface of human tumour cells but do not bind detectably to normal cells, e.g., fibroblasts, endothehial cells or epithelial cells in the major organs. The high biological activity of the chimeric antibodies against human tumour cell lines combined with minimal reactivity with normal tissues implant the man and the man and the contaction of the chimeric in the detection of the minimal reactivity with normal tissues implants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        malignant tissue. The presence of human rather than murine antigenic determinants on the chimeric antibodies increases their resistence to rapid clearance from the body relative to the original murine mAbs. This resistance to clearance enhances the potential utility of these chimeric
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                                                                                                                                                                                                                                                                                     Antibody for detecting antigen in animal or killing cells carrying antigen comprises human constant region and variable region having specificity for human tumor antigen bound by ING-1 antibody
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                                                                                  Chang CP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 444 BP; 109 A; 122 C; 94 G; 119 T; 0 other;
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                                                                                  Lei
                                                                              Robinson RR,
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(XOMA ) XOMA TECHNOLOGY LTD
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GATATCCAGATGACACAGACTACATCCTCCTGTCTGCCTCTCTGGGAGACAGAGTCACC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 ATCAGTTGCAGGGCAAGTCAGGACATTAGTAATTATTTAAACTGGTATCAACAGAAACCA 180
                                                                                                                                                                                            Human, antibody, interleukin-6; receptor; IL-6R; light chain; L; H; heavy chain; variable region; mouse; monoclonal; hybridoma; AUK146-15; plasmid; p146k3; p146-h1; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Argerierccacaccreaerrecrirecrecreergarcrerrrrcaaggraccagarer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequences given in AAQ30759 and AAQ31337 were used in example to illustrate the production of a human antibody which recognises human interleukin-6 receptor (IL-6R). The antibody comprises light (L) chain and heavy (H) chain variable regions which were derived from a mouse monoclonal antibody produced from the hybridoma AUK146-15 which (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGGTGTCCTCAGCTCCTTGGTCTCCTGTTGCTCTGTTTTCAAGGTACCAGATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               has low antigenicity and contains mouse V-region complementarity determining regions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reconstituted human antibody to human interleukin-6 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tsuchiya M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 381 BP; 106 A; 90 C; 86 G; 99 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sato K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, Page 127-128, 207pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saldanha JW,
                                                                                                                                                                                                                                                                                   Location/Qualifiers
421 GGCACCAAACTGGAAATCAA 440
                                                                   ВР.
                                                                  AAQ30759 standard; cDNA; 381
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Conservative
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(first entry)
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61..381
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Matches 357; Conserv
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30-MAR-1993
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sig_peptide
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                                         RESULT 13
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AAQ12061 standard; DNA; 402
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                                                                       Similarity 93.2
54; Conservative
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(GREC ) GREEN CROSS CORP.
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to treat such diseases.
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15-AUG-1991
                                                                                     Matches 354;
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Best Local S
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                               181 GATGGAACTGTTAAACTCCTGATCTACGATACATCAAGATTACACTCAGGAGTCCCATCA 240
                                                                                          241 AGGTTCAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAGCAACCTGGAGCAA 300
                                                                                                                                    301 GAAGACATTGCCACTTACTTTTGCCAACAGGGTAACACGCTTCCGTACACGTTCGGAGGG 360
                                                                                                                                                       The present sequence encodes the light chain variable region of the murine anti-human interleukin 5 receptor alpha chain (NIL-5R alpha) monoclonal antibody (MAD) KM1259. KM1259 is produced by the hybridoma FERM BP-5134, which was prepared by immunising Balb/c mice with HIL-5R alpha, fusing spleen cells obtained from the mice with mouse myeloma P3-U1 cells and screening the resultant hybridomas. The MAD can be used to detect or assay for hIL-5R alpha and cells expressing it on their surface, especially to diagnose allergic respiratory diseases, e.g. chronic bronchitis. It can also be used
               GATGGAACTATTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA
                                                                          AGGTTCAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAACAACCTGGAGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibody against alpha-chain of human interleukin 5 receptor -
useful for diagnosis and treatment of respiratory allergic diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                     Complementarity determining region; CDR; light chain, treatment, variable region; murine; mouse; human; interleukin 5; IL-5; receptor; alpha chain; monoclonal antibody; hybridoma; detection; assay; diagnosis; allergic respiratory disease; chronic bronchitis; da
                                                                                                                                                                                                                                                                                                                                                                                          cDNA encoding light chain variable region of KM1259 antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Koike M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Iida A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Pages 122-123; 238pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                               GGGACCAAGCTGGAAATAAA 380
                                                                                                                                                                                                               || ||||||| ||||||| || GGCACCAAGTTGGAAATCAA 380
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                                                                                                                                                                                                                                                                                                      AAT73611 standard; cDNA; 382 BP
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Takatsu K;
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Nakamura K,
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                                                                                                                                                  1 ATGATGTCCTCTGCTCAGTTCCTTGGTCTCCTGTTTTTCAAGATATCAGATGT
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                                                                                                                                                                                                                                                                                                121 ATCAGTTGCAGGCAAGTCAGGACATTAGCAGTTATTTAAACTGGTATCAGCAGAAACCA
                                                                                                                                                                                                                                                                                                                                                                                                         GAAGACATTGCCACTTACTTTTGCCAACAGGGTAACACGCTTCCGTACACGTTCGGAGGG
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                                                                                                                            1 ATGGTGTCCTCAGCTCCGTTGGTCTCCTGTTGCTCTGTTTTCAAGGTACCAGATGT
                                                                                   Gaps
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0
                                         DB 18; Length 382;
                        Score 338.4; DB 18; _____
Pred. No. 1.8e-95; ____rnches 26; Indels
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Seguence 382 BP; 102 A; 89 C; 90 G; 101 T; 0 other;
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                                                                                0; Mismatches
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22..402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202 GATGGAACTGTTAAACTCCTGATCTATTACACATCAAGTTTACACTCAGGAGTCCCATCA 261
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                                                                                                                               This sequence encodes the light (kappa) chain variable (V) region of a mouse monoclonal antibody (MAb), 1C11, specific for an HIV-1 viral antigen. It is used in the construction of a chimeric MAb comprising heavy and light chains having murine V regions and human C regions. The chimeric MAbs are more effective than murine MAb IC11 since they have an increased compatibility in humans. The heavy and light chain V-regions are joined by manipulating their respective joining (J) regions, to generate restriction enzyme conjugates, in association with e.g. toxins for HIV treatment.
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                                    to detect, kill and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.6%; Score 333.6; DB 12; Length 402; 92.4%; Pred. No. 5.7e-94; ive 0; Mismatches 29; Indels 0;
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                                                                                                                                                                                                                                                                                                                                They can also be used in diagnosis of HIV.
See also AAQ12056-60 and AAQ12056-63.
(Updated on 25-WAR-2003 to correct PA field.)
(Updated on 25-WAR-2003 to correct PI field.)
(Updated on 25-WAR-2003 to correct PI field.)
                                  New chimeric mouse-human antibodies - used remove {\rm HIV}\textsc{-1} antigen from sample
                                                                                            Disclosure; fig 13; 107pp; English
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Best Local Similarity 92.4
Matches 351, Conservative
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Search completed: October 24, 2003, 03:57:07 Job time : 191.538 secs

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Title: Perfect score:

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Minimum DB 8 Maximum DB 8

Database

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BQ918407. 1459 bp mRNA linear EST 20-AUG-2002
AGENCOURT 8885602 NCI CGAP Co24 Mus musculus cDNA clone
IMAGE:6397382 5', mRNA sequence.
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Musiaes 1 to 1459)
I (bases 1 to 1459)
NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
Email: cagabb-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
fromd through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM13895 row c column: 15
High quality sequence start: 165
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BF581392
AZ311392
BC3563548
BC356354
BC3581840
BU899295
AW40553
CB986317
CB986317
CB986632
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 BQ918407 AGENCOURT
BI152061 602916512
BF123422 601760623
B1455041 603173343
                                                                                                                        October 24, 2003, 03:39:05 ; Search time 1673.61 Seconds (without alignments) 5532.953 Million cell updates/sec
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               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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381
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seq length: 200000000
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88.9
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85.9
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Score

No. Result

339.4 338.6 336.8 327.2

BF580940 602100035 BF580940 602100036 BF580940 602101109 BF123744 601766491 BF231341 1M0016K06 BG963548 602831226 CB958057 AGENCOURT BW899295 AGENCOURT BW899295 AGENCOURT CB98631 AGENCOURT CB98631 AGENCOURT CB98631 AGENCOURT CB986236 AGENCOURT CB956236 AGENCOURT CB956236 AGENCOURT CB95623070 602245105 BF664472 602144635 AW406866 U1-HF-BLO CB95633970 602253071 CB95643 AGENCOURT CB95633970 602553071 CB96644 AGENCOURT CB95633970 AGENCOURT CB95633970 AGENCOURT CB956330 AGENCOURT

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Email: cgapbs-r@mail.nih.gov
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602916512F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5066931 5',
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                                                                             /grain="rvb.v"
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Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI CGAP Library."
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Mamaalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinae; Mus-
I (Dases 1 to 827)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                           1 ATGGTGTCCTCAGCTCCAGTTCCTTGGTCTCCTGTTGCTCTGTTTTCAAGGTACCAGATGT
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89.1%; Score 339.4; DB 13;
Best Local Similarity 93.2%; Pred. No. 7.2e-94;
Matches 355; Conservative 0; Mismatches 26; I
                           1. 1459
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/mol_type="mRNA"
/strain="FVB/N"
ity sequence stop: (
Location/Qualifiers
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BF123422 669 bp mRNA linear EST 24-OCT-2000 601760623F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:4023749 5',
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Stem cell origin."
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/site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
Library constructed by Life Technologies. Investigator
providing samples: Gibbert Smith, NIH"
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATCAGTTGCAGGGCAAGTCAGGACATTAGCAGTTATTTAAACTGGTATCAGCAGAAACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               193 AGATGGAACTGTTAAACTACTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.9%; Score 338.6; DB 12; Length 827; 94.8%; Pred. No. 9.6e-94; ive 0; Mismatches 19; Indels 1;
Found through the I.M.A.G.E. Consortium/LLNL
                http://image.llnl.gov
Plate: LLAMIl180 row: h column: 04
High quality sequence stop: 827.
Location/Qualifiers
                                                                                                                                                      /organism="Mus musculus"
                                                                                                                                                                               /mol_type="mRNA"
/strain="CZECH II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360 GGGGACCAAGCTGGAAATAAA 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 361; Conservative
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708 bp mRNA linear EST 26-JUN-2001
602889345F1 NCI CGAP_Kid14 Mus musculus cDNA clone IMAGE:5044690
5', mRNA sequence.
BI103114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 ATCAATTGCAGGGCAAGTCAGGACATTACCAATTATTTAAATTGGTATCAGCAGAAACCA 185
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                                                                                                                                                                             Email: cgapbs_remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAMISS row: e column: 12
High quality sequence stop: 820.
Location/Qualifiers
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                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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/organism="Mus musculus"
                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="tumor, gross tissue"
/dev stage="7" months"
/lab_host="DH10B"
/clone lib="NMIC CGAP_Mam5"
/note="Organ: mammary; Vector: pCNV-SPORT6; Site_1: Sal1;
Site_2: Not!; Cloned unidirectionally. Primer: Gliso dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATGACACAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACCATCAGTTG 120
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM9282 row: n column: 06
High quality sequence stop: 649.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157
                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/mol_type="mRNA,"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="IMAGE:4023749"
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Best Local Similarity 94.1%;
Matches 350; Conservative
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                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLAMI1122 row: i column: 11

High quality sequence stop: 706.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 AATGICCAGATGACACCACACACCTCCCCTGTCTCCCTCTCTGGGAGACAGAGTCACC 131
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Average insert size 1.75 kb. Constructed by Life
Technologies Note: this is a NCI_CGAP Library. |"
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                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 708)
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                                                                                                                       TMT-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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                                     Mus musculus (house mouse)
   GI:14554007
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                                                       Mus musculus
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Matches 344; Conserv
   BI103114.1
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Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I Lo 73. I Lo 73. I Lo 73. I Lo 73. I Nath-WG Chttp://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC.clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLAM99813 row: g column: 09

High quality sequence stop: 694.
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81.9%; Score 312; DB 10;
Best Local Similarity 90.5%; Pred. No. 1.6e-85;
Matches 344; Conservative 0; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
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Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
78 a 153 c 137 g 158 t
                                                                                                              BFS82283 626 bp mRNA linear EST 12-DEC-2000 602101109F1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4224267 5',
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                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 626)
                                                                                                                                                                                                                                                                                                                                                                                                                      L Unpublished
Contact: Robert Strausberg, Ph.D.
Email: gapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey B. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9814 row: a column: 04
High quality sequence stop: 624.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GATATCCAGATGACACCAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 ATCAGTTGCAGGGCAAGTCAGGACATTAGCAGTTATTTAAACTGGTATCAGCAGAAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 ATCAATTGCAGTGCAAGTCAGGGCATTAGCAATTATTTAAATTGGTATCAGCAGAAACCA
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                  Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                           BF582283.1 GI:11655995
370 CACCAAGGTGGAAGTCA 386
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                                                                                                                                                                 mRNA sequence.
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Best Local S
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                                         BF578083 966 bp mRNA linear EST 12-DEC-2000 C020947591 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4209015 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dlab_host="IMAGE:4209015"
/lab_host="DH10B (T1 phage-resistant)"
/clone lib="NCI CGAP_CO24"
/note="Dogan: colon; Vector: pCMV-SPORT6; Site_1: Not1;
/note="Colong unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I toses 1 to 96.
NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9774 row: e column: 16
High quality sequence stop: 614.
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92.3%; Pred. No. 8.9e-85;
ive 0; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
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                                                                                                                                                                                  Mus musculus (house mouse)
Mus musculus
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Matches 348; Conservative
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                                                                                               mRNA sequence.
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RESULT 7
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Mammalia, Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musmalia; Eutheria; Rasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, M., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Quackenbuch, G., Schrimil, L.M., Kanapin, A., Mateuda, H., Batalov, S., Baisel, K.W., Blake, J.A., Bradat, D. Bult, C., Hume, D.A., Basisl, K., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Vons, Jarvis, E.D., Konagaya, A., Kurochkin, I.V., Lee, Y., Lehnard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Perrovsky, N., Pillai, R., Pontius, J.U., Oi, D., N., Ramachandran, S., Ravasi, T., Reed, D.J., Carming, B.C., Rangla, M., Shimada, K., Sultana, R., Taylor, M.S., Tasadale, R., Wells, C., Wenno, H., Nakamue, M., Sakazume, N., Sandellin, A., Schneider, C., Semple, C., Wanagisawa, M., Sakazume, N., Sandellin, R., Maraki, K., Kawai, J., Alzawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Zinner, A., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Shinagawa, A., Wanninci, P., Hayatsu, I., Miyazaki, A., Hashizume, W., Ishinagawa, A., Yasunishi, A., Sakai, A., Lander, K., Shinagawa, A., Wanning, P., Hayatsu, I., Wasunishi, A., Yasunishi, A., Sakazuma, A., Kara, Yasunishi, A., Yas
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan
1-7-22 Suchiro-cho, Teurumi-ku, Good, Japan
1-7-22 Suchiro-cho, Teurumi-ku, Japan
1-7-22 Suchiro-cho, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY235531 BYEN full-length enriched, adult inner ear Mus musculus cDNA clone F930042F10 5', mRNA sequence.
264 CTCTCACCATTAGCAACCTGGAGCAAGAAGATA-TGCCACTTACTTTTGCCAACAGGGTA 322
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Nature 420, 563-573 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
                                                                                                                                                                                                                                                                            323 AAGCGCTTCCTCGGACGTTCGGTGGAGGCACCAAGGTGGAAATCAA 368
                                                                                                                                                                         335 ACACGCTTCCGTACACGTTCGGAGGGGGGGCCAAGCTGGAAATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
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/db xref="taxx".
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/clone="IMAGE:4023550"
/dev stage="taxx".
/dev stage="numbrs"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam5"
/clone_lib="NCI_CGAP_Mam5"
/clone_lib="NCI_Cloned unidirectionally. Primer: Öligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 774)
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Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9282 row: e column: 23
High quality sequence stop: 736.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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78.8%; Score 300.4; DB 10; Length 774;
Best Local Similarity 93.6%; Pred. No. 6.6e-82;
Matches 324; Conservative 0; Mismatches 21; Indels 1;
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/mol_type="mRNA"
/strain="C57BL/6J"
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sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                       prepare mouse tissues.

Tissues were provided by Kirk W. Beisel (Boys Town National Research Hospital 555 North 30th Street Omaha,NE 68131 USA) whose assistance we gratefully acknowledge. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

Location/Qualifiers
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (Daces 1 to 772)
NIH-MG chttp://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/tissue type="inner ear"
/dev_stage="adult"
/clone_lib="RIKEN full-length enriched, adult inner ear"
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Contact: Robert Strausberg, Ph.D.
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lucuring musculus"

/ organism="Mus musculus"
/mol_type="mRNA"
/strān="FVBAN"
/db_xref="tusxon:10090"
/clone="IMAGE:4219618"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NCI CGAP_CO24"
//note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Not1;
//note="Organ: colon; Vector: pCMV-SPORT6; Not2; Not2; Title: Not2; Title: Not2; Title: Not2; Title: Not2; Not2; Title: No
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. Mouse whole genome scaffolding with paired end reads from 10kb
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Tissue Procurement: Jeffrey E. Green, M.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) Sequencing by: The I.M.A.G.E. Consortium (LLNL) Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.lln.gov. o column: 11 High quality sequence stop: 715. High quality sequence stop: 715.
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Pred. No. 3.6e-80;
0; Mismatches 38; Indels 0;
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Best Local Similarity 89.3
Matches 317; Conservative
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Mus musculus (house mouse)
Mus musculus
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                                                                                                                                          mRNA sequence.
402 CTCCCAC 396
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Best Local 1
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ORIGIN
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TITLE
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COMMENT
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BG963548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pw02 (gi|4732114|gb|RR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL110-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                    SIC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      462 TCAGCAACCTGGAACCTGAAGATATTGCCACTTACTATTGTCAGCAGTATAGTTAAGCTTC
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                                                                                                Biomedical Polymers Research Bldg., 20 S. 2030 E.,
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                                                                                                                                                                                                Insert Length: 10000 Std Error: 0.00 Plate: 0016 row: K column: 06 Seq primer: CGTTGTAAACGACGGCGAGT Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                           organism="Mus musculus"
                                   Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Rese
84112, USA
                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0016K06"
                                                                                                                                                                                                                                                                                High quality sequence stop: 730.
Location/Qualifiers
                                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 90.99
Matches 279; Conservative
plasmid inserts
Unpublished
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BG963548 12-JUN-2001
602831226F1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4985791 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 AGGTTCAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAACAACCTGGAGCAA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          256 AGGITCAGIGGCAGIGGGICTGGGICAGAITAITCICTCACCAICAGCAGCCTAGAGTCT 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      316 GAAGATTÍTGCAGACTÁTTACTGTCTÁCÁACGTGATGCGTATCCGTGGACGTTCGGTGGC 375
                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 714)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="DHIOB (TI phage-resistant)"
/close lib="NOI CGAP CGA"
/close lib="NOI CGAP CGA"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo d'
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 ATCAGGGCTCCTGCTCAGTTTCTTGGCATCTTGTTGCTGTCTTCCAGGTGCTCTAGGTATCCAGGTGTCAGATGT
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                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-remail.nih.gov
Tissue procurement: Jeffrey E. Green, M.D.
Tissue procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can lfound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMN0994 row. c column: 08
High quality sequence stop: 712.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="IMAGE:4985791"
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/lab host="DH10B (phage-resistant)"
/clone lib="NIH MGC_113"
/clone lib="NIH MGC_113"
/clone lib="NIH MGC_113"
/note="Corgan: spleen; Vector: pOTB7; Site_1: Xho1; Site_2: DecR1; cDNA made by oling-dT priming. Directionally cloned into EcoR1/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CONA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BQ881840 888 bp mRNA linear EST 16-AUG-2002
AGENCOURT 8642888 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6295725
5', mRNA Fequence.
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                                                            219 GGGAAAGCCCCTAAACTCCTGATCTATACTGCATCCACTTTGCAAGGTGGAGTCCCATCA 278
                                                                                                                                                                                                                                                          279 AGGTTCAGTGGCAGTGGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 338
                                                                                                                                                                                                                                                                                                                                                      GAAGACATTGCCACTTACTTTTGCCAACAGGGTAACACGCTTCCGTACACGTTCGGAGGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                     339 GAAGATTITGCAACTTACTACTGTCAGCAGATTACAGAAACCCGTTCACTTTCGGCGGA 398
181 GATGGAACTATTAAACTCCTGATCTACTACATCAAGATTACACTCAGGAGTCCCATCA 240
                                                                                                                                                                      241 AGGITCAGIGGCAGIGGGICIGGAACAGAITAITCICICACCAITAACAACCIGGAGCAA 300
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 888)
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Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC.clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCMS502 row: g column: 22
High quality sequence stop: 655.
Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 7e-64;
0; Mismatches 86; Indels
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/db_xref="taxon:9606"
/clone="IMAGE:6295725"
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Best Local Similarity 77.4%;
Matches 294; Conservative
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TITLE
JOURNAL
COMMENT
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KEYWORDS
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/db xref="taxon:9606"
/clone="INARA"
/lab host="DH10B (T1 phage-resistant)"
/clone="INARA"
/clone="INARA"
/clone="INARA"
/clone="DH10B (T1 phage-resistant)"
/clone="DH10B (T2 phage-resistant)"
/clone="DH10B (T
                                                                                                                                                                                                                                                                                                                                        CB958057 762 bp mRNA linear EST 29-APR-2003 AGENCOURT 13785358 NIH_MGC_184 Homo sapiens cDNA clone MRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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NIH-MGC http://mgc.nci.nih.gov/.
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CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM148 row: g column: 15
High quality sequence stop: 558.
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77.4%; Pred. No. 6.5e-64;
ive 0; Mismatches 86; I
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                                                                                                                             376 GGCACCAAGCTGGAAATCAA 395
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                                              GGGACCAAGCTGGAAATAAA
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VERSION
                                                                                                                                                                                                                                                              RESULT 14
CB958057
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AUTHORS
TITLE
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SOURCE
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임 8 75

76 GACATCCAGATGACCCAGTCTCCATCCTCCTGTCTGCATCTGTAGGAGACAGAGTCACC 135

Search completed: October 24, 2003, 05:48:28 Job time : 1680.61 secs

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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 381 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Washington STATE: D.C.
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STREET: 30
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Sequence 36,
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1 ATGTGTCCTCAGCTCAGTT......GGACCAAGCTGGAAATAAAT 381
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                  GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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US-08-436-717-28
US-08-26-520-1
US-08-458-516-4
US-08-458-516-4
US-08-458-516-4
US-08-458-516-4
US-08-458-516-4
US-08-436-717-36
US-08-436-717-36
US-08-436-717-36
US-08-436-51-28
US-08-448-51-28
US-08-454-683-5
US-08-454-683-5
US-08-454-683-5
US-08-454-683-5
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US-08-438-528-19
US-08-438-562-19
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US-08-836-561-102
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US-08-836-561-91
US-09-434-122-70
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length
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APPLICANT: SATO, Koh
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
CORRESPONDENCE: 158
CORRESPONDENCE: 158
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COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FLING DATE: 20-DEC-1993
FLING DATE: 24-DEC-1993
PRIOR APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION NUMBER: D4 + 32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, HATCAIC C.
REGISTRENCE/DOCKET NUMBER: 53,258
REFERENCE/DOCKET NUMBER: 53,258
REFERENCE/DOCKET NUMBER: 53,258
REFERENCE/DOCKET NUMBER: 53,258
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PCT-US95-05262-3
US-08-040-204-13
US-08-040-204-15
US-08-040-204-16
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US-08-121-054C-29
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US-08-040-204-12
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US-09-813-659-29
US-08-403-853-17
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Patent No. 5795965
GENERAL INFORMATION:
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3000 K Street, N.W.
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
FLING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                              100.0%; Score 381; DB 1; L
100.0%; Pred. No. 4.5e-112;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 28, Application US/08436717;
Patent No. 5817790
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
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                                                                                                                                                                               Best Local Similarity 100.
Matches 381; Conservative
                                                                                               mat_peptide
STRANDEDNESS: single
TOPOLOGY: linear
                                                                1..381
                                            NAME/KEY:
LOCATION:
FEATURE:
                                                                                               ; NAME/KEY:
; LOCATION:
US-08-137-117D-28
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                                                                                                                                                                 Query Match
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181 GATGGAACTATTAAACTCCTGATCTACTACATCAAGATTACACTCAGGAGTCCCATCA 240
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Similarity 100.0%; Pred. No. 4.5e-112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP FEB1-1992
FILING DATE: 19-FEB1-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY AGENT: INFORMATION:
NAME: WEGNER, HAIOLI C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 33466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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Patent No. 5591629
GENERAL INFORMATION:
APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
TITLE OF INVENTION: MONOCLONAL A
                                                                                                                                                                                                                                                                                                                                                                        (202) 672-5300
(202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 381 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 381; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-436-717-28
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US-08-236-520-1
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Best Local S
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180 240

120

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360

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LOCATION:
PCT-US95-05262-1
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    CENTRAL NERVOUS SYSTEM REMYELINATION
                                                                                                                                                                                  COMPUTER FLADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/236,520
FLING DATE: 29-APR-1994
ATTONEY/AGENT INFORMATION:
NAME: GRANAHAIN:
REFERENCE/DOCKET NUMBER: 27,227
REFERENCE/DOCKET NUMBER: 27,227
REFERENCE/DOCKET NUMBER: MAV92-01
TELECOMMUNICATION INFORMATION:
TELEFRAK: 617-861-6240
TELEFRAK: 617-861-6340
TITLE OF INVENTION: CENTRAL NERVOUS SYSTEM REMYEL NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smithy & Reynolds, STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 GGGACCAAGCTGGAAATAAA 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 96.6
Matches 367; Conservative
                                                                                                       CITY: Lexington
STATE: Massachusetts
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LOCATION:
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61 GATATCCAGATGACACAGACTACATCCTCCCTGTCTGCCCCTCTCTGGGAGACAGAGTCACC 120
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APPLICANT: Mayo Foundation for Medical Education Research
TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH PROMOTE
TITLE OF INVENTION: CENTRAL NERVOUS SYSTEM REMYELINATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                              NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smithy & Reynolds, P.C.
STREET: How Militia Drive
CITY: Lexington
STATE: Massachusetts
                                                                                                                                                                                                                   ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYER: FLOPBY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: PCT/US95/05262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 359.2; DB 5;
Pred. No. 4e-105;
0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: U.S. 08/236,520
FILING DATE: April 29, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Particia
REGISTRATION NUMBER: 27,227
REFERENCE/DOCKET NUMBER: MAV92-01 PCT
TELEPHONE: 617-861-6240
TELEPHONE: 617-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGACCAAGCTGGAAATAAA 380
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96.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 393 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 96.6'
Matches 367; Conservative
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                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361
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; Sequence 1, Application PC/TUS9505262 ; GENERAL INFORMATION:

PCT-US95-05262-1

RESULT 4

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301 GAAGATATTGCCACTTACTTTTGCCAACAGGGTAATACGCTTCCGTGGACGTTCGGTGGA 360
                                                                                                                                                                                                                                                                                      APPLICANT: MITJANS, Francesc
APPLICANT: MITJANS, Francesc
APPLICANT: PIULATS, Jaume
APPLICANT: ROSELL, Elisabet
APPLICANT: ADAN, Jaumen
APPLICANT: GOODNAN, Simon
APPLICANT: HAHN, Diane
TITLE OF INVENTION: Anti-alpha-V-Integrin Monoclonal
TITLE OF INVENTION: Antibody
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/574,699A
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: EP 94120165.9
FILING DATE: 20-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hamlet-King, Diana
REGISTRATION NUMBER: 33,302
REGISTRATION NUMBER: 33,302
REGISTRATION NUMBER: 33,302
REGISTRATION NUMBER: 33,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 2200 Clarendon Blvd. CLITY: Arlington STATE: VA
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LOCATION: 1..60
OCHER INFORMATION: /function= "Leader sequence"
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 61..381
                                                                                                                                                                                                                       ; Sequence 1, Application US/08574699A
; Patent No. 5985278
; GENERAL INFORMATION:
                                                               361 GGGACCAAGCTGGAAATAAA 380
                                                                                                        361 GGCACCAAGCTGGAAATCAA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: MERG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6433
TELEFAN: 703-243-6410
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 381 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1..381
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HYPOTHETICAL: NC
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72-17E6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE
CLONE: 72-17E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 ATCAGTTGCAGGCAAGTCAGGACATTAACAATTATTTAAACTGGTATCAGCAGAAACCA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 381;
                                                                                                   APPLICANT: CO. Man Sung
APPLICANT: TSO, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIIB/IIIA
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE: ADDRESSE: ADDRESSEE: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
FILING DATE:
CLASSIFICATION 1424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTOOREY/AGENT INPORMATION:
NNAME: GATE: WAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 351.2; DB 1;
Pred. No. 1.4e-102;
0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11823-37-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFRENCE/DOCKET NUMBER: 11823
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2402
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 381 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
                                    Sequence 4, Application US/08458516
Patent No. 5777085
GENERAL INFORMATION:
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Best Local Similarity 95.3%;
Matches 362; Conservative
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; LOCATION:
US-08-458-516-4
                US-08-458-516-4
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AGGTTCAGTGGCAGTGGGACTGGAACAGATTATTCTCTCACCATTAACAACCTGGAGCAA 300
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TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN NUMBER OF SEQUENCES:

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner STREET:

STREET: 3000 K Street; N.W., Suite 500
CITY: Wachington
CITY: Wachington
STREET: D.C.

COUNTRY: USA
ZIP: 20007-5109
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 19-FEB-1992
PRIOR APPLICATION NUMBER: JP 4-32084
FILING DATE: 25-APR-1991
RTING DATE: 25-APR-1991
ATTORNEY APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY APPLICATION NUMBER: 25,258
REGISTRATION NUMBER: 25,258
REGISTRATION NUMBER: 25,258
REPERENCE/DOCKET NUMBER: 25,259
REPERENCE/DOCKET NUMBER: 25,258
REPERENCE/DOCKET NUMBER: 25,259
REPERENCE/DOCKET NUMBER: 25,258
REPERENCE/DOCKET NUMBER: 25,259
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TELEX: 904136
INPORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 94.5
Matches 359; Conservative
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US-08-137-117D-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GATATCCAGATGACACAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAGACATTGCCACTTACTTTTGCCAACAGGGTAACACGCTTCCGTACACGTTCGGAGGG 360
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Pred. No. 9.5e-102;
0; Mismatches 19; Indels 0
                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 208.7228
OTHER INFORMATION: /function= "CDR-2 sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 325. 351
OTHER INFORMATION: /function= "CDR-3 sequence"
                                                                                                             FEATURE:
NAME/KEY: misc_feature
LOCATION: 130..162
OTHER INFORMATION: /function= "CDR-1 sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature

LOCATION: 352..381

CTHER INFORMATION: /function= "FR-4 sequence"

MS-08-574-6994-1
                                   NAME/KEY: misc feature
LOCATION: 61..129
OTHER INFORMATION: /function= "FR-1 sequence"
                                                                                                                                                                                                      FEATURE:
NAME/KEY: misc_feature
LOCATION: 163..207
OTHER INFORMATION: /function= "FR-2 sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: 229.7324
OTHER INFORMATION: /function= "FR-3 sequence"
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Patent No. 5795965
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: SATO, Koh
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGACCAAGCTGGAAATAA 379
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95.0%;
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Best Local Similarity
Matches 360; Conserva
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180

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Best Local Similarity 94.5%; Pred. No. 4.8e-101;
Matches 359; Conservative 0; Mismatches 21;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM COM
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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US-08-836-561-28
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                                          GAAGACATTGCCACTTACTTTTGCCAACAGGGTAACACGCTTCCGTACACGTTCGGAGGG 360
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APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Wary
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TILING DATE: US/US/150//17

CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: J9 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: J9 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGISTRATION NUMBER: 25.258
REFERENCE/DOCKET NUMBER: 25.258
REFERENCE/DOCKET NUMBER: 25.258
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: Washington STATE: D.C. COUNTRY: USA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                              361 GCCACCAAGTTGGAAATCAA 380
                                                                                                                                                                                                                       Sequence 36, Application US/08436717 Patent No. 5817790
                                                                                           361 GGGACCAAGCTGGAAATAAA 380
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INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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NAME/KEY:
LOCATION:
US-08-436-717-36
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90.9%; Score 346.4; DB 1; Length 381;

Query Match

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300
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Gaps
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APPLICANT: FURUYA, Akiko
APPLICANT: INDA, Akihiro
APPLICANT: INDA, Akihiro
APPLICANT: HANZAWA, Hideharu
APPLICANT: HANZAWA, Hideharu
APPLICANT: HANZAWA, No. 6018032uo
APPLICANT: HANZAY, No. 6018032uo
APPLICANT: HANZAY, No. 6018032uo
APPLICANT: HANZAY, No. 6018032uo
APPLICANT: HANZAY, No. 6018032uo
APPLICANTION: Receptor Alpha Chain
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
Indels
21;
                                                     1 ATGGTGTCCTCAGCTCAGTTCCTTGGTCTCCTGTTGCTC
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REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT ING SYSTEM: DOS
SOFTWARE: FASTSEM: DOS
SOFTWARE: FASTSEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,561
FILING DATE: 09-MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: JP 232384/95
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: LAWYENCE IT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
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Patent No. 6018032
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TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: KOIKE, Masamichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Diskette
IBM Compatible
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TOPOLOGY: linear MOLECULE TYPE: cDNA SEQUENCE DESCRIPTION: SEQ ID NO: US-09-434-122-28
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No. 5750078th Glebe Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: HANAI, No. 5750078uo APPLICANT: HASEGAWA, Mamoru APPLICANT: MIYAJI, Hiromasa APPLICANT: KUWANA, Yoshihisa TITLE OF INVENTION: Process for PITILE OF INVENTION: Antibody NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGACCAAGTTGGAAATAAA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 GGGACCAAGCTGGAAATAAA 380
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; Patent No. 5750078
                                                                                                                                                                                                                                                                     LENGTH: 382 base pairs
                                                                                                                                                                                                  TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: singl
                  PRIOR APPLICATION DATA:
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APPLICANT: SHITARA, Kenya
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Best Local Similarity
Matches 354; Conserv
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STREET: NO
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US-08-408-133-5
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FURUYA, Akiko
NAKAMURA, Kazuyasu
IIDA, Akihiro
ANAZAWA, Hideharu
HANAI, No. 6538111uo
TAKATSU Kiyoshi
TITLE OF INVÉNTION: Antibody Against Human Interleukin-5
                                                                                                                                                                                   Length 382;
                                                                                                                                                                                                                   26; Indels
                                                                                                                                                                                   DB 3;
                                                                                                                                                                                   Score 338.4; DB 3
Pred. No. 1.7e-98;
0; Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPATER: BM Compatible
COMPATE: PSSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
RENT APPLICATION DATA:
FILING DATE: 05-NO. 6538111-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 28, Application US/09434122 Patent No. 6538111 GENERAL INFORMATION:
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                                    28:
                                                                                                                                                                                 88.8%;
93.2%;
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2
SEGUENCE CHARACTERISTICS:
LENGTH: 382 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM
                                                                                                                                                                                                                  Matches 354; Conservative
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                                                                                                                                                                                                     Similarity
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US-09-434-122-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 AGGITCAGIGGCAGIGGGICIGGAACAGAITAITCICICACCAITAACAACCTGGAGCAA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAGACATTGCCACTTACTTTTGCCAACAGGGTAACACGCTTCCGTACACGTTCGGAGGG 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 382;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.8%; Score 338.4; DB 4
93.2%; Pred. No. 1.7e-98;
Live 0; Mismatches 26
                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
REFERNCE/DOCKET NUMBER: 7005-115-999
TELECOMMUNICATION INFORMATION:
APPLICATION NUMBER: 08/836,561
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: 1P 232384/95
FILING DATE: 11-SEP-1995
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325 GAAGATATTGCCACTTACTTTTGTCATCAGTATAGTAAGCTTCCGTGGACGTTCGGTGGA 384
                                                                                                                                                                                                               Sequence 5, Application US/08454683
Parent No. 5807548
PAPLICANT: SHITARA, Kenya
APPLICANT: HANAI, No. 5807548uo
APPLICANT: HASEGAMA, Mamoru
APPLICANT: MIYAJI, Hiromasa
APPLICANT: KUWANA, YOSHIMISA
TITLE OF INVENTION: Process for Producing Humanized Chimera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Nixon & Vanderhye, P.C.
STREET: No. 5807548th Glebe Road
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
RPLICATION UNMBER: US/08/454,683
FILING DATE: 31-MAY-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 31-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US/08/408,133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
APPLICATION NUMBER: US 08/292,178
FILING DATE:
APPLICATION NUMBER: US 07/947,674
FILING DATE: 17-SEPT-1992
ATTORNEY/AGENT INFORMATION:
                                               361 GGGACCAAGCTGGAAATAAA 380
                                                                                              385 GGCACCAAGCTGGAAATCAA 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNET CRAWFORD, Arthur R
TELECOMMUNICATION INFORMATION:
TELEFHONE: (703)816-4000
TELEFAX: (803)816-4100
TELEFX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 408 base pairs
TYPE: nucleic acid
STRANDENESS: double
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OTHER INFORMATION:
FEATURE:
NAME/KEY: 819_peptide
LOCATION: 25..84
OTHER INFORMATION:
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LOCATION: 85..408

COTER INFORMATION:

05.08-454-683-5
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & V
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HYPOTHETICAL: N
ORIGINAL SOURCE:
STRAIN: KM-641
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                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,178
FILING DATE: US 07/947,674
FILING DATE: 17-SEPT-1992
ATTORNEY/AGENT INFORMATION:
NAME: CRAMPORD, Arthur R
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPACOM (703)816-4100
TELEFAX: (803)816-4100
TELEFAX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 408 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                    US/08/408,133
                                                                                                                                                          SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/408.17
                      COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: N
ORIGINAL SOURCE:
STRAIN: KM-641
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Best Local Similarity 90.5
Matches 344; Conservative
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LOCATION: 25...84
OTHER INFORMATION:
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LOCATION: 85.408
OTHER INFORMATION:
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OTHER INFORMATION:
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61 GATATCCAGATGACACAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACC 120
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Patent No. 6437098
APPLICANT: SHITNRA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAMA, MAMORU
APPLICANT: MIYALI, HIROMASA
APPLICANT: KUWANA, YOSHHIHSA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
PILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/09/225,322B
CURRENT FILING DATE: 1999-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 322.4; DB 2;
Pred. No. 2.2e-93;
0; Mismatches 36;
FILING DATE: 18-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: SADOFP, B.J.
REGISTRATION NUMBER: 36,663.
REFERENCE/DOCKET NUMBER: 249-74
TELECOMMUNICATION INFORMATION:
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 408 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOOULGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 GGGACCAAGCTGGAAATAAA 380
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Best Local Similarity 90.5%;
Matches 344; Conservative
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85..408
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25..84
                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CDNA FEATURE:
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LOCATION:
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LOCATION:
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, LOCATION:
US-08-454-680-5
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US-09-225-322B-9
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                                                                                                                                                                                                                                            85 GATATCCAGATGACACAGACTGCATCCTCCTGCCTGCTCTGGGAGACAGAGTCACC 144
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                                                                                                                                                 84
                                                                                                    1 ATGGTGTCCTCAGCTCCAGTTCCTTGGTCTCCTGTTGCTCTGTTTTCAAGGTACCAGATGT
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GENERAL INFORMATION:

APPLICANT: SHITARA, KENYA

APPLICANT: HANAI, NOBUO

APPLICANT: HASEGAWA, MAMORU

APPLICANT: HASEGAWA, MAMORU

APPLICANT: MIXAI, HIROMSA

TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA

TITLE OF INVENTION: ANTIBODY

NUMBER OF SEQUENCES:

ADDRESSEE: NIXON & VANDERHYE P.C.

STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR

CITY: ARLINGTON

STATE: VA

COUNTY: USA
    Query Match

84.6%; Score 322.4; DB 1; Length 408;
Best Local Similarity 90.5%; Pred, No. 2.2e-93;
Matches 344; Conservative 0; Mismatches 36; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYEE FILDEP GLEAR
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,680
FILING DATE: 31-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/408,133
FILING DATE: 21-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,178
FILING DATE: 17-AUG-1994
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/947,674
FILING DATE: 17-AUG-1992
PRIOR APPLICATION NUMBER: US 07/947,674
FILING DATE: 17-SEP-1992
PROR APPLICATION NUMBER: US 07/947,674
FILING DATE: 17-SEP-1992
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US-08-454-680-5
'Sequence 5, Application US/08454680
'Patent No. 5866692
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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Patent No. 649566
GENERAL INFORMATION:
APPLICANT: SHITARA, KERYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGARA, MAWORU
APPLICANT: MYSAJI, HIROMASA
APPLICANT: KUWANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REPREMENCE: 249-101
CURRENT APPLICATION NUMBER: US/09/764,304
CURRENT FILING DATE: 2001-01-19
                                                                                                                                                                                                                                                                                                          CTHER INFORMATION: Description of Artificial Sequence:cDNA KM-641
NAME/KEY: CDS
LOCATION: (25)..(408)
NAME/KEY: mat peptide
LOCATION: (85)..(408)
NAME/KEY: sig_peptide
LOCATION: (25)..(84)
US-09-225-122B-9
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Pred. No. 2.2e-93;
0; Mismatches 36;
PRIOR FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/408,133
PRIOR PELING DATE: 1995-03-21
PRIOR FILING DATE: 1994-08-17
PRIOR FILING DATE: 1994-08-17
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR APPLICATION NUMBER: US 07/947,674
PRIOR FILING DATE: 1992-09-17
PRIOR FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATCHTIN VET: 2.0
SEQ ID NO 9
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90.5%;
                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 90.5
Matches 344; Conservative
                                                                                                                                                                                                                                     LENGTH: 408
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US-09-764-304-9
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Pred. No. 2.2e-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 36; Indels
EARLIER FILING DATE: 1999-01-05
EARLIER APPLICATION NUMBER: US 08/454,680
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER FILING DATE: 1995-05-31-21
EARLIER FILING DATE: 1995-03-21
EARLIER FILING DATE: 1994-08-17
EARLIER FILING DATE: 1994-08-17
EARLIER FILING DATE: 1992-09-17
EARLIER APPLICATION NUMBER: US07/947,674
EARLIER APPLICATION NUMBER: US07/947,674
EARLIER APPLICATION NUMBER: US07/947,674
EARLIER APPLICATION NUMBER: US07/947,674
EARLIER FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 9
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Job time : 58.8788 secs
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 90.5
Matches 344; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: (25)..(408)
NAME/KEY: mat peptide
LOCATION: (85)..(408)
NAME/KEY: sig peptide
LOCATION: (25)..(84)
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300

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RESULT 1
US-08-779-784-20
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Sequence 4, Appli
Sequence 1, Appli
Sequence 28, Appl
Sequence 9, Appli
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Sequence 97, Appl
Sequence 70, Appl
Sequence 91, Appl
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Sequence 9, Appli
GENERAL INFORMA
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                                                                                                                          October 24, 2003, 03:57:16 ; Search time 904.875 Seconds (without alignments) 1129.179 Million cell updates/sec
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Sequence 22, A
Sequence 3, A
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2. / cgn2_6/ptodatea/2/pubpna/USO6_NEW_PUB.seq:*
3. / cgn2_6/ptodatea/2/pubpna/USO6_NEW_PUB.seq:*
3. / cgn2_6/ptodatea/2/pubpna/USO6_NEW_PUB.seq:*
4. / cgn2_6/ptodatea/2/pubpna/USO6_PUBCOMB.seq:*
5. / cgn2_6/ptodatea/2/pubpna/PCTUS_PUBCOMB.seq:*
7. / cgn2_6/ptodatea/2/pubpna/USO8_NEW_PUB.seq:*
7. / cgn2_6/ptodatea/2/pubpna/USO8_NEW_PUB.seq:*
8. / cgn2_6/ptodatea/2/pubpna/USO8_PUBCOMB.seq:*
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10. / cgn2_6/ptodatea/2/pubpna/USO8_PUBCOMB.seq:*
11. / cgn2_6/ptodatea/2/pubpna/USO8_PUBCOMB.seq:*
12. / cgn2_6/ptodatea/2/pubpna/USO8_NEW_PUB.seq:*
13. / cgn2_6/ptodatea/2/pubpna/USO8_PUBCOMB.seq:*
14. / cgn2_6/ptodatea/2/pubpna/USO8_PUBCOMB.seq:*
15. / cgn2_6/ptodatea/2/pubpna/USO8_NEW_PUB.seq:*
16. / cgn2_6/ptodatea/2/pubpna/USO8_NEW_PUB.seq:*
16. / cgn2_6/ptodatea/2/pubpna/USO8_NEW_PUB.seq:*
16. / cgn2_6/ptodatea/2/pubpna/USO8_PUBCOMB.seq:*
17. / cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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2 US-10-010-729-63
2 US-10-268-883-4
4 US-10-283-349-28
US-10-283-349-28
US-10-10-283-349-10
US-10-10-265-713-9
US-10-283-349-102
US-10-283-349-97
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US-10-283-349-97
US-10-283-349-97
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Maximum Match 100%
Listing first 45 summaries
                                                                                  - nucleic search, using sw model
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Match
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Perfect score:
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338.4
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ALIGNMENTS

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MCS-08-779-784-20

1 Sequence 2.0. Application US/08779784

1 Publication No. US20020164325A1

2 GENERAL INFORMATION:

3 APPLICANT: Redirguez, Moses

3 APPLICANT: Adaktura, Kunihiko

1 TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM

1 TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM

1 TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM

1 TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM

1 TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM

1 TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM

1 TITLE OF INVENTION: PROMOTION USING MONOCLONAL AUTOANTIBODIES

1 CORRESPONDENCE ADDRESS:

2 TITLE OF INVENTION: BATCH

3 TREET: Hook Jersey

1 CONFUTRY: USA

2 TITLE New Jersey

2 CONFUTRY: USA

2 TITLE OF STEET PROME:

3 MEDIUM TYPE: Plopy disk

COMPUTER REDABLE FORM:

4 MEDIUM TYPE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/779, 784

FILING DATE: 08-AUG-1996

PRICAR PAPLICATION NUMBER: US 08/692,084

FILING DATE: 08-AUG-1996

PROME PATION NUMBER: US 08/236,520

FILING DATE: 29-AFR-1994

ATTORNEY APPLICATION NUMBER: 26,742

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 199-1-001 CIPA

TELECOMMUNICATION INFORMATION:

1 REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA

TELECOMMUNICATION INFORMATION:

1 TELECOMMUNICATION INFORMATION:

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Publication No. US20030138862A1
GENERAL INFORMATION:
APPLICANT: Tso, J. Yun
APPLICANT: Green, Jennifer Macphate
TITLE OF INVENTION: Anti-HIA-DR Antibodies and the Methods of Using Thereof
FILE REPRENCE: 05882.0062.NPUS01
CURRENT APPLICATION NUMBER: US/10/268,883
CURRENT FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: US/80 60/329,178
PRIOR APPLICATION NUMBER: US/80 60/331,965
PRIOR FILING DATE: 2001-11-21
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                                                                                                                                                      Length 393;
                                                                                                                                                                                              Indels
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                                                                                                                                                Score 359.2; DB 12;
Pred. No. 1.4e-110;
0; Mismatches 13; I
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Pred. No. 6.6e-108;
0; Mismatches 18; 1
  FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 GGGACCAAGCTGGAAATAAA 380
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
                                                                                                                                                  Query Match

Best Local Similarity 96.6%;
Matches 367; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 95.3
Matches 362; Conservative
                                                                                      ORGANISM: Mus musculus
US-10-010-729-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , ORGANISM: Mouse US-10-268-883-4
SOFTWARE: Fast
SEQ ID NO 63
LENGTH: 393
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                                                                  TYPE: DNA
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Sequence 63, Application US/10010729

Publication No. US20030185827A1

GENERAL INPORMATION:

GENERAL INPORMATION:

APPLICANT: Miller, David 3.

APPLICANT: Place Larry R.

TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous TITLE OF INVENTION: MANBER: US/10/10,729

CURRENT APPLICATION NUMBER: US/10/11-13

PRIOR PELING DATE: 2000-12-05

PRIOR APPLICATION NUMBER: 09/730,473

PRIOR APPLICATION NUMBER: 09/730,739

PRIOR PELING DATE: 1999-05-28

PRIOR PELING DATE: 1999-05-28

PRIOR FILING DATE: 1999-05-28

PRIOR FILING DATE: 1999-06-28

PRIOR FILING DATE: 1994-04-29

PRIOR FILING DATE: 1994-04-29
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                                                                                                                                                                                                                                                                                   Length 393;
                                                                                                                                                                                                                                                                                   Score 359.2; DB 8; Length
Pred. No. 1.4e-110;
0; Mismatches 13; Indels
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                   INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS: LENGTH: 393 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear
                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 96.6%;
Matches 367; Conservative
    201-343-1684
                                                                                                                                                                                                                       1..393
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US-08-779-784-20
                                                                                                                                                                                                 NAME/KEY:
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US-10-010-729-63
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121 ATCAGTTGCAGGGCAAGTCAGGACATTAGCAGTTATTTAAACTGGTATCAGCAGAAACCA 180
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93.2%; Pred. No. 1.4e-103;
tive 0; Mismatches 26; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                     NAKAMURA, Kazuyasu
IIDA, Akihiro
ANAZAWA, Hidana, Hida
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REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/283,349
FILLING DATE: 29-Oct-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/836,561
FILLING DATE: 09-MAY-1997
APPLICATION NUMBER: JP 232384/95
FILING DATE: 11-SEP-1995
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SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-10-283-349-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTER Version 2.0
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TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                      Sequence 28, Application US/10283349
Publication No. US20030096977A1
GENERAL INFORMATION:
                                                                                          361 ĠĠĊŔĊĊŔŔĠĊŢĠĠŔŔŖĊŔŔ 380
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: KOIKE, Masamichi
FURUYA, Akiko
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INFORMATION FOR SEQ ID NO: 28
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COMPUTER READABLE FORM
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Best Local Similarity
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                                                                                                                          121 ATCAGTTGCAGGTCAAGTCAGGACATTAGCAAATATTTAAACTGGTATCAGCAGAAACCA 180
                                                                                                                                                                                                         240
                                                                                                                                                                                                                                                            GATGGAACTGTTAAACTCCTGATCTACAACATCAAGATTACACTCAGGAGTCCCATCA 240
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GATAICCAGAIGACACAGACTACAICCTCCCIGICTGCCICICIGGGAGACAGAGICACC 120
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                                                                                                                                                                                                         GATGGAACTATTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA
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Pred. No. 2.3e-107;
0; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: NAGATA, Shigekazu
APPLICANT: YATOMI, Takehiro
APPLICANT: YOMI, Takehiro
APPLICANT: SUDA, Takehiro
TITLE OF INVENTION: PROPHYLACTIC/THERAPEUTIC AGENT
FILE REFERENCE: 1110-0307P
CURRENT APPLICATION NUMBER: US/10/084,139
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGACCAAGCTGGAAATAAA 380
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Publication No. US20030109416A1
GENERAL INFORMATION:
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95.0%;
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SEQ ID NO 1
LENGTH: 381
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US-10-084-139-1
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US-10-084-139-1
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APPLICANT: SHILMEN, NENUA
APPLICANT: HANAI, NORUA
APPLICANT: HANAI, NORUA
APPLICANT: HASEGAMA, MAMORU
APPLICANT: MIXAI, HIROMASA
APPLICANT: MIXAI, HIROMASA
APPLICANT: MIXAI, HIROMASA
APPLICANT: KUWANA, YOSHHISSA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT FILING DATE: 2090-01-05
PRIOR FILING DATE: 1990-01-05
PRIOR PLICATION NUMBER: US 08/454,680
PRIOR FILING DATE: 1995-05-31
PRIOR FILING DATE: 1995-05-31
PRIOR FILING DATE: 1995-03-21
PRIOR FILING DATE: 1995-08-17
PRIOR FILING DATE: 1992-09-17
PRIOR FILING DATE: 1992-09-17
PRIOR FILING DATE: 1992-09-17
PRIOR FILING DATE: 1992-09-17
PRIOR FILING DATE: 1991-08-17
PRIOR FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 9
TENNORM AND 9
                                                                                                                                                                             AGGTTCAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAACAACCTGGAGCAA
                                                                                                                                                                                                                                                                                              265 AGGTTCAGTGGCGGTGGGTCCGGGACAGATTATTCTCTCACCATCAGCAACCTGGAGCCT
                                                                                                 145 ATCAGTTGCAGTGCAAGTCAGGACATTAGTAATTATTTAAACTGGTATCAACAGAAACCA
                                                                                                                                                                                                                                                                                                                                             GAAGACATTGCCACTTACTTTGCCAACAGGGTAACACGCTTCCGTACACGTTCGGAGGG
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                                                    121 ATCAGTTGCAGGGCAAGTCAGGACATTAGCAGTTATTTAAACTGGTATCAGCAGAAACCA
                                                                                                                                                 181 GATGGAACTATTAAACTCCTGATCTACAACATCAAGATTACACTCAGGAGTCCCATCA
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OTHER INFORMATION: Description of Artificial Sequence:cDNA KM-641
FEATURE:
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Pred. No. 3.5e-98;
0; Mismatches 36; I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.6%;
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Best Local Similarity 90.55
Matches 344; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: mat_peptide LOCATION: (85)..(408)
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LOCATION: (25)..(84)
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LOCATION: (25)..(408)
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181 GATGGAACTGTTGAACTCCTGATCTACCACATCAAGATTACAGTCAGGAGTCCCATCA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/09764304

Sequence 9, Application US/09764304

Sequence 9, Application US/09764304

Sequence 9, Application US/09764304

Septemation US/0020026036a1

APPLICANT: BAITARA, KENVA

APPLICANT: HANAI, NOBUO

APPLICANT: HANAI, NOBUO

APPLICANT: KUWANA, YOSHIHISA

TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY

FILE REFERENCE: 249-101

CURRENT APPLICATION NUMBER: US/09/764,304

CURRENT APPLICATION NUMBER: US/09/25,322

EARLIER APPLICATION NUMBER: US 08/25,322

EARLIER FILING DATE: 1999-01-05

EARLIER FILING DATE: 1999-01-05

EARLIER FILING DATE: 1999-03-21

EARLIER PILING DATE: 1994-08-17

EARLIER PILING DATE: 1994-08-17

EARLIER FILING DATE: 1994-08-17

EARLIER FILING DATE: 1994-08-17

EARLIER FILING DATE: 1991-09-18

NUMBER: OF SEQ ID NOST: 19

SOFTWARE: PALCATION NUMBER: US 07/947,674

EARLIER FILING DATE: 1991-09-18

NUMBER: OF SEQ ID NOST: 19
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Pred. No. 3.5e-98;
0; Mismatches 36;
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                                                                                                                                                                                                                                                                                                                                                                      361 GGGACCAAGCTGGAAATAAA 380
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Best Local Similarity 90.5%;
Matches 344; Conservative
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LOCATION: (85)..(408)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: sig peptide LOCATION: (25)..(84)
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LENGTH: 408
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85 GATATCCAGATGACACAGACTGCATCCTCCCTGCCTCTCTGGGAGACAGAGTCACC 144
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                                                                                                                                                                                                                                                                                                                 GATATCCAGATGACACAGACTACATCCTCCCTGTCTGCCTCTCGGGAGACAGAGTCACC
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       84.6%; Score 322.4; DB 14; Length 408; 90.5%; Pred. No. 3.5e-98; ive 0; Mismatches 36; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HANAI, NOBUO
KUWANA, YOSHIHISA
HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FALON APPLICATION UNMBER: US/09/393,385B FILING DATE: 27-UDA-96 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/10/195,752
FILING DATE: 16-Uul-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                          1 ATGGTGTCCTCAGCTCAGTTCCTTGGTCTCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
US-10-195-752-19
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
KOIKE, MASAMICHI
SHITARA, KENYA
CHITARA, CHITA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FELEPHONE: (703)816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 GGGACCAAGCTGGAAATAAA 380
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                                           Best Local Similarity 90.5
Matches 344; Conservative
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           Query Match
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                                                                                                                      GATATCCAGATGACACAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACC 120
                                                                                                                                                                      GATATCCAGATGACACAGACTGCTCCCTGCCTGCTCTCTGGGAGACAGAGTCACC 144
                                                                                                                                                                                                                                                                     121 ATCAGTIGCAGGGCAAGTCAGGACATTAGCAGTTATTTAAACTGGTATCAGCAGAAACCA 180
                                                                                                                                                                                                                                                                                                                 GATGGAACTATTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA 240
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Sequence 9, Application US/10265713
Fublication No. US20030095964A1
GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HARSEARA, MANCRU
APPLICANT: HARSEARA, MANCRU
APPLICANT: HARSEARA, MANCRU
APPLICANT: HARSEARA, WINDRITON PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILLE REFERENCE: 449-101
CURRENT APPLICATION NUMBER: US/10/265,713
CURRENT APPLICATION NUMBER: US/09/225,322
FRIOR FILING DATE: 1999-01-06
FRIOR FILING DATE: 1995-05-31
FRIOR FILING DATE: 1995-05-31
FRIOR FILING DATE: 1995-03-21
FRIOR FILING DATE: 1994-08-17
FRIOR FILING DATE: 1994-08-17
FRIOR FILING DATE: 1994-08-17
FRIOR FILING DATE: 1992-09-18
FRIOR FILING DATE: 1992-09-18
FRIOR FILING DATE: 1992-09-18
FRIOR FILING DATE: 1991-09-18
FRIOR PRIOR APPLICATION NUMBER: US 08/292,178
FRIOR PRIOR FILING DATE: 1991-09-18
FRIOR PRIOR PRESENTED ATE: 1991-09-18
FRIOR PRIOR APPLICATION NUMBER: US 08/292,178
FRIOR APPLICATION NUMBER: US 08/292,178
FRIOR PRIOR FILING DATE: 1991-09-18
FRIOR PRIOR PRIOR DATE: 1991-09-18
FRIOR PRIOR DATE: 1991-09-18
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: sig_peptide;
; LOCATION: (25)..(84)
US-10-265-713-9
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NAME/KEY: CDS
LOCATION: (25)..(408)
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APPLICANT: KOIKE, mec.
NAKAMURA, Kazuyasu
IIDA, Akihiro
ANAZAWA, Hideharu
HANAZWA, Hideharu
HANAI, No. US20030096977Aluo
TAKATSU, Kiyoshi
TITLE OF INVENTION: Antibody Against Human Interleukin-5
Receptor Alpha Chain
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0
                                                                                                                                                                                                               Length 382;
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                                                                                                                                                                                                                    DB 14;
                                                                                                                                                                                                                 Score 309.6; DB 1.
Pred. No. 6.9e-94;
); Mismatches 44
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 29-Oct-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
               SEQUENCE CHARACTERISTICS:
LENGTH: 382 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other
SEQUENCE DESCRIPTION: SEQ ID NO: 102:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         380
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Publication No. US20030096977A1
GENERAL INFORMATION:
APPLICANT: KOIKE, Masamichi
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INFORMATION FOR SEQ ID NO: 102
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88.4%;
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Matches 336;
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                           25 ATGATGTCCTCTGCTCAGTTCCTTGGTCTCCTGTTGCTCTTTTTCAAGGTACCAGATGT
                                                                                  61 GATATCCAGATGACACAGACTACATCCTCCCTGTCTGCCTCTGGGAGACAGAGTCACC
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FURUYA, Akiko
NAKAMURA, Kazuyasu
IIDA, Akihiro
ANAZAWA, Hideharu
HANAI, No. US20030096977Aluo
TAKATSU, Kiyoshi
OF INVENTION: Antibody Against Human Interleukin-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Lawrence, III, Stanton T
REGISTRATION UNDRER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
TELECOMMUNICATION INFORMATION:
TELEFRAX: 212-790-9090
TELEFAX: 212-869-9141
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskete
COMPUTER: IBM Compatible
COMPATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,10/283,349
FILING DATE: 29-OCt-2002
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/836,561
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: UP 232384/95
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the A
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 102, Application US/10283349
Publication No. US20030096977A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGACCAAGCTGGAAATAAA 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 106
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
US-10-283-349-102
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DB 14;
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Pred. No. 3.4e-91;
0; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 7005-115-999
TELECOMMUNICATION INFORMATION:
                                                                                                                     CURRENT TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/283,349
FILING DATE: 29-Oct-2002
CLASSIFICATION ATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/836,561
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 23284/95
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
           STREET: 1155 Avenue of the Americas CITY: New York STATE: NY COUNTRY: USA
ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: Other
SEQUENCE DESCRIPTION: SEQ ID NO: 70:
                                                                                                                                                                                                                                                                                                                                                                                   NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
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                                                                                                          COMPUTER READABLE FORM:
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Best Local Similarity 87.1
Matches 331; Conservative
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US-10-283-349-91
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FURUYA, AKIKO
NAKAMURA, Kazuyasu
IIDA, Akihiro
ANAZAWA, Hideharu
HANAI, NO. US20030096977Aluo
TAKATSU, Kiyoshi
TITLE OF INVENTION: Antibody Against Human Interleukin-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 304.8; DB 1-
Pred. No. 2.9e-92;
0; Mismatches 47
                                                                                                                         NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/836,561
                                                                  APPLICATION NUMBER: JP 232384/95
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: Other SEQUENCE DESCRIPTION: SEQ ID NO: 97:
                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 70, Application US/10283349
Publication No. US20030096977A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                        LENGTH: 382 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                   TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 97:
                                                                                                                                                                                                                                                                                                                                                                                                                                        80.0%;
                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 80.0
Best Local Similarity 87.6
Matches 333; Conservative
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US-10-283-349-70
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61 GATATCCAGATGACACAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACC 120 GAAGACATIGCCACTIACTITIGCCAACAGGGTAACACGCTICCGTACACGTICGGAGGG 360 121 ATCAGTTGCAGGCAAGTCAGGACATTAGCAGTTATTTAAACTGGTATCAGCAGAAACCA 180 181 GATGGAACTATTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA 240 GGGAAAGCCCCTAAGCTCCTGATCTACCACACAAGATTACAGTCAGGAGTCCCATCA 240 241 AGGTTCAGTGGCAGCGGGTCTGGAACAGATTTCACTCTCACCATTAGTAGTCTGCAACCT 300 GAAGATTTTGCCACTTACTACTGCCAACAGGGTTATACGCTTCCGTACACGTTCGGCCAA 360 9 9 1 Argargrecrerecreatrecrregrerecretrecretrireaagarareagarer 1 ATGGTGTCCTCAGCTCCAGTTCCTTGGTCTCCTGTTGCTCTGTTTCAAGGTACCAGATGT Gaps ; 0 Indels

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0
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Publication No. US20030096977A1
GENERAL INFORMATION:
APPLICANT: KOIKE, Masamichi
FURUYA, Akiko
NAKAMURA, Kazuyasu
IIDA, KAhihiro
ANAZAWA, Hideharu
HANAI, No. US20030096977Aluo
TAKATSU, Kiyoshi
TITLE OF INVENTION: Receptor Alpha Chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 300; DB 14; Length 382;
Pred. No. 1.2e-90;
0; Mismatches 50; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATGGTGTCCTCAGCTCCAGTTCCTTGGTCTCCTGTTGCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 7005-115-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/283,349
FILIMG DATE: 29-Oct-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/836,561
PLING DATE: 09 + MAY-1997
APPLICATION NUMBER: UP 232384/95
FILING DATE: 11-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: Other
SEQUENCE DESCRIPTION: SEQ ID NO: 87:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
                                                                                                                                                     361 GGGACCAAGCTGGAAATAAA 380
                                                                                                                                                                                          361 GGGACCAAGGTGGAAATAAA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78.7%;
86.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 87
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COUNTRY: USA
ZIP: 10036
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Matches 330; Conserv
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Query Match
Pest Local Similarity 87.1%; Pred. No. 3.4e-91;
Matches 331; Conservative 0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION NUMBER: US/10/283,349
FILING DATE: 29-Oct-2002
CLASSIFICATION: CURKNOWN>
PRIOR APPLICATION: CURKNOWN>
PRIOR APPLICATION NUMBER: US/08/836,561
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US/08/836,561
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: Other
SEQUENCE DESCRIPTION: SEQ ID NO: 91:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 91:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 382 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette
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ZIP: 10036
COMPUTER READABLE FORM:
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US-08-779-784-22

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Search completed: October 24, 2003, 06:22:16 Job time : 908.375 secs
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                                                                                                               181 GGGAAAGCCCCTGAACTCCTGATCTACCACACATCAAGATTACAGTCAGGAGTCCCATCA 240
                                                                                                                                                                                                                                                                                     241 AGGTTCAGTGGCAGCGGGTCTGGAACTTTCACTCTCACCATTAGTAGTCTGCAACCT 300
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    61 GATATCCAGATGACACAGTCTCCATCCTCTGTCTGCCTCTGTAGGAGACAGAGTCACC 120

                                                                                 ATCAGTTGCAGGCAAGTCAGGACATTAGCAGTTATTTAAACTGGTATCAGCAGAAACCA 180
                                                                                                                                                                     181 GATGGAACTATTAAACTCCTGATCTACTACATCAAGATTACACTCAGGAGTCCCATCA 240
                                                                                                                                                                                                                                                              AGGTTCAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAACAACCTGGAGCAA 300
                                                                                                                                                                                                                                                                                                                                                  GAAGACATTGCCACTTACTTTTGCCAACAGGGTAACACGCTTCCGTACACGTTCGGAGGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 22, Application US/08779784
Publication No. US20020164325A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
APPLICANT: Asakura, Kunihiko
TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
TITLE OF INVENTION: REYYELINATION USING MONOCLONAL AUTOANTIBODIES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER KEADABLE FORM:
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,784
FILING DATE: 07-04N-1997
CLASSIFICATION NUMBER: US 08/692,084
FILING DATE: 08-40G-1996
PRIOR APPLICATION NUMBER: US 08/692,084
FILING DATE: 29-AFR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 1199-1-001 CIPA
TELECOMMUNICATION NUMBER: 1199-1-001 CIPA
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                      361 GGGACCAAGCTGGAAATAAA 380
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 324 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
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US-08-779-784-22
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120
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                                                                                                                                                                                                        121 ATCAGTTGCAGGGCAAGTCAGGACATTAGCAGTTATTTAAACTGGTATCAGCAGAAACCA 180
                                                                                                                                                                                                                                                                                                                                                                                                          241 AGGTTCAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAACAACCTGGAGCAA 300
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                                                                                                                                                       9
                                                                                                                                       1 GATATCCAGATGACACAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACC
                                                                                                                                                                                                                                   61 ATCAGTTGCAGGGCAAGTCAGGACATTAGCAATTATTTAAACTGGTATCAGCAGAAACCA
                                                                                                   61 GATATCCAGATGACACAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACC
                                                         Gaps
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     Length 324;
                                                    Indels
  Score 299.2; DB 8;
Pred. No. 2e-90;
0; Mismatches 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 GGGACCAAGCTGGAAATAAA 380
Query Match
Best Local Similarity 95.9%;
Matches 307; Conservative
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Rat immunoglobulin pKM641 LA2 immunog KM641 H chain vari

Murine immunoglobu Ganglioside GD3 sp Modified gangliosi

Title: Perfect score:

Sequence:

protein

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Run δ

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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Ganglioside GD3 sp
anti-CD22 monoclon
Ganglioside GD3 sp
Chimeric 4H6 anti-
Ganglioside GD3 sp
Diphtheria toxin/V
Murine anti-CD3 MA
An immunocoxin com
Recombinant immuno
Diphtheria toxin/V
Diphtheria toxin/V
Diphtheria toxin/V
Mouse C4G1 Ig ligh
Variable region of
MAD VLI7E6 light c
p146-K3 protein pr
Mouse MAD 1011 L c
Light (kappa) Chai
Human/murihe IL-1
                                                                                                                                                                                 Light chain variab
CD19:zeta chimeric
Ganglioside-associ
Ganglioside-associ
Murine consensus 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Mature peptide"
                                                                                                                                                                                  AAW21844
ABB82300
ABJ18571
                                                                                                                                                                                                                          ABJ18574
AAY94216
AAB81999
AAW66098
                                                                                                                                                                                                                                                                                 AAB81994
AAB49242
AAB81995
AAU75368
AAU75369
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AAU75366
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AAU75373
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AAR30768
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AAU75365
AAU75370
AAU75382
                                                                                                                                                       AAY28368
AAR53340
                                                                                                                             ABU11003
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(first entry)
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  pPM-k3 protein product.
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9913.6
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9913.8
9813.8
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9813.8
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30-MAR-1993
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19-FEB-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
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    pPM-k3 protein pro
MAb SCH94.03 light
Anti-CD4 antibody
Mouse anti-thuman F
Mouse antibody F91
ME4 Light Chain V
MAb ME4 light chain
Mouse ME4 light chai
Mouse antibody ligh
                                                                                               October 22, 2003, 22:03:25; Search time 57.2462 Seconds (without alignments) 352.133 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                       A Geneseq 19Jun03:*

| SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDS1/gcgdata/geneseqfy-embl/AA41981.DAT:*
| SIDS1/gcgdata/geneseqfy-embl/AA41981.DAT:*
| SIDS1/gcgdata/geneseqfy-embl/AA41981.DAT:*
| SIDS1/gcgdata/geneseqfy-embl/AA1981.DAT:*
| SIDS1/gcgdata/geneseqfy-embl/AA1981.DAT:*
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| SIDS1/gcgdata/geneseqfy-embl/AA1991.DAT:*
| SIDS1/gcgdata/geneseqfy-embl/AA1992.DAT:*
| SIDS1/gcgdata/geneseqfy-embl/AA1999.DAT:*
| SIDS1/gcgdata/geneseqfy-embl/AA2000.DAT:*
| SIDS1/gcgdata/geneseqfy-embl/AA20
                                                                                                                                                                                  MVSSAQFLGLLLLCFQGTRC......CQQGNTLPYTFGGGTKLEIN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                    1107863
                 GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                       1107863 segs, 158726573 residues
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                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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AAR32121
AAW11815
AAW60033
AAR09426
AAW06215
AAW85062
                                                                       protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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1127
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Match
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Score

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638 627 621 621 621 621

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1 MVSSAQFLGLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
                                                                                                                                                                                                                                                                                             Hybridoma ATCC CRL 11627 was obtd. from a SJL/J mouse injected with spinal cord homogenate from a mammal uninfected with any demyedinating disease. The hybridoma produced a monoclonal antibody (SCH94.03) useful in promoting CNS remyelination. The SCH94.03 light chain amino acid sequence is given in AAR84553.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunosuppression; tissue transplantation; graft; L chain; V region; T-helper cell inhibition; transplant rejection; MAb; interleukin-2 receptor.
                                                                                                                                                                                Monoclonal antibodies which stimulate central nervous system re-myelination - are produced by hybridoma ATCC CRL 11627, for treating multiple sclerosis, and viral or post-neural diseases or
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 638; DB 16; Length 131;
Pred. No. 7.8e-42;
5; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-CD4 antibody MT 15.1 light chain variable region.
                                                                                                                                                                                                                                                                     Disclosure; Page 36-37; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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21..115
/label= Variable
116..127
/label= J2
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96.0%;
 95WO-US05262.
                                  94US-0236520.
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(updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 121; Conservative
                                                                                                  Rodriguez M;
                                                                 (MAYO-) MAYO FOUNDATION
                                                                                                                                   WPI; 1995-393077/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTKLEI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     131 AA;
                                                                                                                                                   N-PSDB; AAT05311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTKLEI
 27-APR-1995;
                                29-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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10-MAR-2003
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                                                                                                  Miller DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                  the CNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                               The sequences given in AAR28670-71 were encoded by plasmids which were used in example to illustrate the production of a human antibody which recognises human interleukin-6 receptor (IL.6R). The antibody which comprises light (L) chain and heavy (H) chain variable regions which were derived from a mouse monoclonal antibody produced from the hybridoma PM1 which contained the plasmids pPM-K3 and pPM-h1. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 DGTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MVSSAQFLGLLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MVSSAQFLGLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monoclonal antibody, MAb, SCH94.03; hybridoma, central nervous syste
CNS, demyelination, multiple sclerosis, neural disease, therapeutic.
                                                                                                                  Reconstituted human antibody to human interleukin-6 receptor - has low antigenicity and contains mouse V-region complementarity determining regions
                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 661; DB 13; Length 127; 100.0%; Pred. No. 1.3e-43; ive 0; Mismatches 0; Indels 0
                                  Tsuchiya M;
                                  Saldanha JW, Sato K,
                                                                                                                                                                                  Disclosure; Page 121-122; 207pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 16. 128
| label = Joining_region
| 129. 131
| label = C-kappa_region
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/label= Leader_peptide
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/label= CDR1
70..76
/label= CDR2
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/label= CDR3
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                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAb SCH94.03 light chain.
(CHUS ) CHUGAI SEIYAKU
                                Bendig MM, Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTKLEIN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GTKLEIN 127
                                                                WPI; 1992-398882/48.
N-PSDB; AAQ30755.
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Sequence

61

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121

AAR84553

Peptide

AAR84553 LID AARR XXX XXX XXX XXX XXX XXX MODE MAD DE MAD XXX XXX XXX XXX XXX XXX XXX PT Regi PT Regi

Region Region Region Region Region

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us-09-114-285a-29.rag

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AAW60033 standard; Protein; 127 AA
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/label= CDR_2
109..117
/label= CDR_3
                                                                                                                                                                                                                                                                                                                                                                        (MOCH ) MOCHIDA PHARM CO LTD. (OSAB-) OSAKA BIOSCIENCE INST
                                                                                                                                                                                                                              96WO-JP01820.
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Best Local Similarity 93.77
Matches 118; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-108917/10.
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                                                                                                                                                                                                                                                                                        17-MAY-1996;
30-JUN-1995;
                                                                                                                     WO9702290-A1
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                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Co MS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DGTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MVSSAQFLGLLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MMSSAQFLGLLLCFQGTRCDIQMTQTISSLSASLGDRVTISCRASQDINNYLSWYQQKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence is the light chain variable region of a preferred anti-CD4 monoclonal antibody for use in the claimed synergistic composition. MAD MT 15.1 is deposited as clone 15-1/P3/14 (ECACC 9009705). The anti-CD4 antibody is used with at least one anti-IL2R alpha or beta antibody. Individually the antibodies are strongly inhibiting and when used together their immunosuppressive properties are improved; they synergistically inhibit T-helper cell proliferation to effectively inhibit transplant rejection at low doses without significantly reducing the general immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                    Synergistic antibody compsn. for use as immunosuppressant -comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R alpha- or anti-IL2R beta antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; Fas ligand, antigen; neutral; antibody; apoptosis; HIV; induction; assay; enzyme linked immunosorbant assay; diagnosis; disease; hepatitis B; hepatitis C; human immunodeficiency virus; graft versus host disease; ulcerative colitis; sequelae; myocardial infarction; mouse; murine; monoclonal; treatment; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 627; DB 14; Length 127;
Pred. No. 5.3e-41;
6; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse anti-human Fas ligand antibody F919 light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                    Scheuer W, Weidle U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                            (BOEF ) BOEHRINGER MANNHEIM GMBH
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/label= CDR_1
70..76
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 9; 18pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tch 94.9%; al Similarity 93.7%; 118; Conservative
     91DE-4143214
                                                          91DE-4124759.
                                                                                                                                                                                                    Kaluza B, Riethmueller G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 AA;
                                                                                                                                                                                                                                                                                        N-PSDB; AAQ36607.
                                                          25-JUL-1991;
30-DEC-1991;
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Best Local (
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61 DGTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MVSSAQFLGLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MMSSAQFLGLLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fas ligand, Fas antagonist, apoptosis related disease, liver disease, heart failure; kidney failure, graft-versus-host disease, antibody; myocardial infarction, ischemic restenosis, endotoxic shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                       Antibody reactive with Fas ligand capable of inducing apoptosis - used for diagnostic assay of Fas ligand in body fluids and for treatment of diseases in which Fas ligand/Fas antigen is involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is the light chain of the mouse anti-apoptosis inducing human Fas ligand, monoclonal antibody, 1919. The antibody can be used in a Fas ligand assay, e.g. an enzyme linked immunosorbant assay, to diagnose diseases in which the Fas ligand/Fas antigen system is implicated, e.g. hepatitis LG, human immunodeficiency virus, garaft/host disorders, ulcerative colitis or sequelae of myocardial infarction. The antibody may also be used to treat such diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.9%; Score 621; DB 18; Length 127; 93.7%; Pred. No. 1.5e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse antibody F919-9-18 light chain sequence.
Shirakawa K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Mismatches
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61 DGTVKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDFATYFCQQGNILPRTFGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence is used in the prodn. of a chimeric antibody mol. comprising two light chains and two heavy chains, each having a constant region (human) and a variable region (murine) having specificity to an antigen bound by murine monoclonal antibody (MAb) ME4. The chimeric antibodies can be used for any purpose for which the original murine MAbs can be used, with the advantage that they are more compatible with the human body. They are esp. used for the diagnosis and treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MVSSAQFLGLLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric mouse-human antibodies - prepd. using genes coding for constant human region murine variable region, esp. to 3 tumour
                               Monoclonal antibody, chimera, light, heavy, chain, constant, variable, antigen, diagnosis, cancer, tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 621; DB 11;
Pred. No. 1.5e-40;
5; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                          Lei S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 13; Page 123 + Fig 29; 173pp; English
                                                                                                                                                                                                                                                                                                                                                                                                          Robinson RR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAb ME4 light chain variable region.
ME4 Light Chain V Region (mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW06215 standard; Protein; 128
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88US-0241744.
88US-0243739.
88US-0253002.
89US-0367641.
                                                                                                                                                                                            89WO-US03852
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                          Horwitz AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1990-115825/15.
N-PSDB; AAQ08608.
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Matches 118; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 AA;
                                                                                      Mus musculus
                                                                                                                                                                                                                                                                               04-OCT-1988;
19-JUN-1989;
21-JUL-1989;
                                                                                                                                                                                          06-SEP-1989;
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13-FEB-1997
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                                                                                                                                                         22-MAR-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This represents the light chain of the mouse antibody F919-9-18. This is used for generating a mouse anti-human Fas ligand monoclonal antibody. The invention provides the use of Fas antagonist as an agent for the treatment and prevention of apoptosis-related diseases. The Fas antagonist can be a partial Fas antigen peptide containing the extracellular part of the protein, but lacking the signal sequence, an anti-Fas antibody, where the antibody is preferably a humanised antibody. The Fas antagonist is used in the treatment and prevention of diseases such as myocardial infarction, heart failure, ischemic heart disease, acute kidney failure, graft-versus-host disease, ischemic restenosis of the heart, liver or kidney, and endotoxic shock, and also as an organ preservative in transplantation. The agent is of low toxicity but effectively inhibits the Fas/Fas ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DGTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DGTVKLLIYYTSRLHSGVPSRFSGSGSGTNYSLTISNLEQGDIATYFCQQGSTLPWTFGG 120
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"complementarity determining region (CDR)
                                "complementarity determining region (CDR)
                                                                   /note= "complementarity determining region (CDR)
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                                                                                                                                                                                                                                                                                                                                                                                                                          Use of Fas antagonist for treatment and prevention of apoptosis-related diseases - such as heart or kidney failure, graft-versus-host disease or liver disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 621; DB 19;
Pred. No. 1.5e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 1; 86pp; Japanese.
                                                                                                                                                                                                                                                                               (MOCH ) MOCHIDA PHARM CO LTD. (OSAB-) OSAKA BIOSCIENCE INST.
                                                                                                                                                                                                                                                                                                                                    Yatomi T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.9%;
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(first entry)
                                                 ..117
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Best Local Similarity 93.7
Matches 118; Conservative
 'note=
                                  /note=
                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-271925/24 N-PSDB; AAV34426.
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                                                                                                                                                                                                                                                                                                                                    Suda T,
                                                                                                      WO9818487-A1
                                                                                                                                                                            31-OCT-1997;
                                                                                                                                                                                                             26-SEP-1997;
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                                                                                                                                         07-MAY-1998
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04-MAR-1993
                                                                                                                                                                                                                                                                                                                                    Nagata S,
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Length 128; Indels

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DGTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DGTVKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDFATYFCQQGNILPRTFGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MVSSAQFLGLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents the light chain variable region of murine antibody ME4. The sequence was used to create chimeric mouse-human immunoglobulins which recognise the human tumour antigen bound by antibody ING-1 (produced by hybridoma cell line ATCC HB 9812). The chimeric antibodies also have an antigen-binding site that competitively inhibits the binding of antibody ING-1, and mediate complement-dependent cytolysis of target cells or antibody-dependent cellular cytocoxicity to target cells. The chimeric antibodies can be used for therapeutic purposes in the
                                                                       Light chain variable region; murine antibody ME4; antibody ING-1; chimeric immunoglobulin; human tumour antigen; chimeric antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric antibody specific for human tumour antigen - useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Robinson RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 621; DB 20;
Pred. No. 1.5e-40;
5; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treatment of human cancer. (Updated on 20-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Horwitz AH, Lei S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunoassay, imaging or antitumour agent
                                   Mouse ME4 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABU58896 standard; Protein; 128 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Fig 29; 92pp; English.
                                                                                                                                                                                                                                                                                                                      910S-0659401.
940S-0364001.
880S-02410624.
88US-0243739.
88US-0253002.
89US-035304.
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Best Local Similarity 93.7%;
Matches 118; Conservative
                                                                                                                                                                                                                                                                    95US-0466034
16-APR-1999 (first entry)
                                                                                                             treatment; human cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Better MD, Chang CP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-044574/04.
N-PSDB; AAV71158.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 AA;
                                                                                                                                                                                                                                                                    06-JUN-1995;
                                                                                                                                                                                       US5843685-A.
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27-DEC-1994;
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19-JUN-1989
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                                                                                                                                                   Mus sp.
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임
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 HMSSAQFLGLLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDITTYLNWYQQKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MVSSAQFLGLLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
               Chimeric antibody; monoclonal antibody; ME4; antibody engineering; tumour; antigen; breast carcinoma; colon carcinoma; lung carcinoma; ovary carcinoma; melanoma; cancer; diagnosis; therapy; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric mouse-human antibodies - recognise a human tumour antigen, used for the treatment and diagnosis of human cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The light chain variable region (AAW06215) of mouse monoclonal antibody ME4 is the product of a CDNA clone (AAT43440) isolated from a ME4 hybridoma cDNA library. MAD ME4 (IgG1) binds to an antigen that is expressed on the surface of human lung, breast, colon and ovary carcinomas and melanomas, but not on most normal adult tissues. The light chain and heavy chain variable regions (see also AAW06216) of ME4 can be linked to human constant regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and expressed in transformed host cells. Novel mouse-human chineric antibodies (see also AAW06209-14 and AAW06217-18) can be produced that have specificity to human tumour antigens for use in the treatment and diagnosis of human cancer.
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93.9%; Score 621; DB 18; Length 128;
Best Local Similarity 93.7%; Pred. No. 1.5e-40;
Matches 118; Conservative 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Robinson RR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lei S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Better MD, Chang CP, Horwitz AH,
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88US-0241744.
88US-0243739.
88US-0253002.
89US-0367641.
89US-0364001.
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N-PSDB; AAT43440.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 AA;
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08-SEP-1988;
13-SEP-1988;
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27-DEC-1994;
                                                                                                                               US5576184-A.
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19-JUN-1989;
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Length 128;

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AAW85062
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AC AAW8
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The invention describes an antibody comprising a human constant region and a variable region having specificity for the human tumour antigen. Cobund by the ING-1 stationdy, where the ING-1 is produced by call line HB9912 as deposited with ATCC, and the antibody has the same affinity as the ING-1 for the human tumour antigen. The antibody is useful in an imaging method for detecting an antigen in a sample by contacting a label and relating the detected label to the presence of the antigen; for use in an imaging method for revealing the presence of a label-detectable containing the antigen; and for killing cells antigen in an animal by contacting the antibody with a part of the animal suspected of containing the antigen; and for killing cells callowing the killing to occur. The antibody and callowing the killing to occur. The antibodies are useful in tumour calls but do not bind detectably to normal cells, e.g., tibroblasts, endothelial cells on the chimeric antibodies against human cumour cells but do not bind detectably to normal cells, e.g., tibroblasts, endothelial cells or epithelial cells in the major organs. The high biological activity of the chimeric antibodies against human cumour cell lines combined with minimal reactivity with normal tissues imply that these antibodies may mediate selective destruction of capanate these antibodies may mediate selective destruction of capanate to clearance enhance the potential utility of these chimeric antibodies, and capanate continents and the body relative to the original murine mabs. This resistance to clearance enhances the potential utility of these chimeric antibodies, and therefore the amino acid sequence of a mouse antibody light chain the antibodies and in the creation of a muchine number them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibody for detecting antigen in animal or killing cells carrying antigen comprises human constant region and variable region having specificity for human tumor antigen bound by ING-i antibody
                                                                                                                                                                                                               Mouse; human tumour antigen; anti-human tumour antigen-antibody; ING-1 antibody; cell line HB9812; immunoassay; imaging; tumour diagnosis; tumour therapy; cytostatic; light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chang CP;
                                                                                                                                                Mouse antibody light chain variable region #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lei S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Robinson RR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Fig 29; 101pp; English.
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94US-0364001.
88US-0240624.
88US-0241744.
88US-0253073.
89US-0357641.
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                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-196707/19.
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06-SEP-1989;
27-DEC-1994;
                                                                      16-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US6461824-B1
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ABU58896;
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                                                     DGTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGG
                                          1 MVSSAQFLGLLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
                       Gaps
                                                                                                                                                                                                                                                                                                          Immunoglobulin; L-chain; platelet membrane glycoprotein; GPIIa/IIIb;
monoclonal antibody; platelet agglutination; humanised antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This is the sequence of the mouse C4G1 immunoglobulin light chain. See AAR39266 for the heavy chain sequence. The antibody is specific for the GPIIa/IIIb protein and inhibits platelet agglutination. The Ig is thus useful in the treatment of thrombosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Compsn. contg. immunoglobulin specific for the GP-IIB and -IIIA protein - for treating disorders related to vascular thrombosis
 Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                              l= complementarity_determining_region_1
                      Indels
Score 621; DB 24;
Pred. No. 1.5e-40;
; Mismatches 3;
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22..127
/label= light_chain
                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Fig 2A, 54pp, Japanese.
                                                                                                                                                                                                            AAR39265 standard; Protein; 127 AA.
                      5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= CDR_2
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/label= CDR_3
 93.9%;
93.7%;
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                                                                                                                                                                                                                                                     (updated)
(first entry)
                                                                                                                                                                                                                                                                                  Mouse C4G1 Ig light-chain.
Query Match
Best Local Similarity 93.7°
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     44..54
/label=
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N-PSDB; AAQ45662.
                                                                                                                                121 GTKLEI 126
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29-NOV-1993
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11-SEP-1992;
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                                                                                                                                                                                                                                                                                                                                          Synthetic
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/label= CDR1
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/label= C
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Best Local Similarity 92.9
Matches 117; Conservative
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/label= (
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/label=
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                                                 rhis is the
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                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                        DGTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGG 120
                                                                                                                                     09
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                                                                                                                                                                   1 MMSSAQFLGFLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDINNYLNWYQQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse, antibody C4G1, light chain; humanised; immunoglobulin; Ig; inhibition; antigen; cardiovascular disease; thromboembolic disorder; cancer; acute myocardial infarction; unstable angina; stroke; transient ischemic episode; pulmonary embolism; deep vein thrombosis; extracorporeal cardiopulmonary circulation.
                                                                                                                                   1 MVSSAQFLGLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New humanised immunoglobulin which binds GPIIb/IIIa - derived from mouse C4G1 antibody, used for inhibiting platelet aggregation for treating cardiovascular and thromboembolic disorders.
                                                                                                 .
0
                                                                   Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "complemetarity determining region"
109..117
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/note= "complemetarity determining region"
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                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Variable region of mouse antibody C4G1 light chain.
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                                                               Score 619; DB 14;
Pred. No. 2.2e-40;
6; Mismatches 3;
(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                             AAW49809 standard; Protein; 127 AA.
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                                                                 93.6%;
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92US-0895952.
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(first entry)
                                                                               al Similarity 92.9
117; Conservative
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N-PSDB; AAV36741.
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                                 127 AA;
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09-JUN-1992;
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24-SEP-1998
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                                 Sequence
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                                                                 Query Match
Best Local
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Protein
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                                                                                   chain, used in the method of the invention involving the creation of a humanised in the method of the invention involving the creation of a humanised ig seapable of binding to GPID/IIIa and inhibiting platelet aggregation and also the releasing reaction of platelets. The Ig can be used for treating cardiovascular diseases and thromboembolic disorders, e.g. acute mycoardial infarction, unstable angina, stroke, transient ischemic episodes, deep vein thromboeis and pulmonary embolism, extraocrporeal cardiopulmonary circulation. The Ig can also be used in diagnosing the presence and location of a thrombus, or certain types of cancer cells which develop GPID/IIIa on their surfaces, for the detection of GPIIb/IIIa antigens or for isolating platelets.

(Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MVSSAQFLGLLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                           amino acid sequence of the mouse antibody C4G1 light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 619; DB 19;
Pred. No. 2.2e-40;
6; Mismatches 3;
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/label= Framework region 1
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/label= Framework region
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/label= Framework
Disclosure; Fig 2A; 35pp; English
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The sequences given in AAR29010-11 were encoded by plasmids which were used in example to illustrate the production of a human antibody which recognises human interleukin-6 receptor (IL-6R). The antibody which comprises light (L) chain and heavy (H) chain variable regions which were derived from a mouse monoclonal antibody produced from the hybridoma AUK146-15 which contained the plasmids p146-k3 and p146-h1. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MVSTPQFLGLLVICFQGTRCDIQMTQTTSSLSASLGBRVTISCRASQDISNYLNWYQQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MVSSAQFLGLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
                                                                                                                                                                                                                Reconstituted human antibody to human interleukin-6 receptor has low antigenicity and contains mouse V-region complementarity determining regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.6%; Score 599; DB 13; Length 127; 90.5%; Pred. No. 7.5e-39;
                                                                                                                               Tsuchiya M;
                                                                                                                               Sato K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Mismatches
                                                                                                                                                                                                                                                                                     Disclosure; Page 127-128; 207pp; Japanese.
                                                                                                                                 Saldanha JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR12237 standard; Protein; 126 AA
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              92WO-JP00544.
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92JP-0032084
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(first entry)
                                                                                               (CHUS ) CHUGAI SEIYAKU KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 114; Conservative
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(GREC ) GREEN CROSS CORP.
(ZOMA-) ZOMA CORP.
                                                                                                                                 Jones ST,
                                                                                                                                                                WPI; 1992-398882/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTKLEI 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 AA;
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              24-APR-1992;
                                            25-APR-1991;
19-FEB-1992;
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19-AUG-1991
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                                                                                                                                 Bendig MM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 DGTVKLLIFYTSKLHSGVPSRFSGSGSGTDYSLTISNLDQEDIATYFCQQGNTFPYTFGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;
heavy chain; variable region; mouse; monoclonal; hybridoma; AUK146-15;
plasmid; p146-k3; p146-h1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MVSSAQFLGLLLLCFQVTRCDIQMTQTTSSLSASLGDRVIISCRASQDISNYLSWYQQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MVSSAQFLGLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
                                                                                                                                                                                                                                                                                  A monoclonal antibody which reacts only with the alphaV chain of human alphaV integrins; which blocks attachment of alphaV integrin bearing cells to integrin substrate; which reverses established cell matrix interactions caused by alphaV integrin; which blocks tumour development and which has no cytotoxic activity, may be used to treat tumours, especially melanoma (but also glioma, carcinoma) optionally coupled to a cytokine such as interleukin-2. The monoclonal antibody may also be used for diagnostic imaging of tumours and assesment of tumour growth when conjugated to a radio opaque-agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                  oĘ
                                                                                                                                                                                New human integrin V chain-specific monoclonal antibody - and related DNA and hybridomas, for treatment and diagnostic imaging
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                                                                               Mitjans F, Piulats J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR29010 standard; Protein; 127 AA.
                                                                                                                                                                                                                                                   Claim 8; Figure 17a; 54pp; English
                                                                               Hahn D,
              94EP-0120165
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(first entry)
                                             (MERE ) MERCK PATENT GMBH.
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Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          p146-k3 protein product.
                                                                                                                                                                                                                    tumours, esp melanoma.
                                                                                                                               WPI; 1996-302345/31.
N-PSDB; AAT35050.
                                                                               Goodman S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTKLEI 126
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              20-DEC-1994;
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                                                                                               Rosell E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                             Adan J,
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                                                                                                                                                                                                                                                                              1 MMSSAQFLGLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCSASQGISNYLNWYQQKP 60
                                                                                                                                                                                                                                                                 1 MVSSAQFLGLLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
                                                                                                                                                                                                                                              Gaps
                                                                                                         The mouse VL gene product may be used to produce chimeric mouse-
human Abs against HIV-1 comprising human Ig constant regions and
murine variable regions. These novel sequence are useful in
treatment, diagnosis and prophylaxis of HIV infections, and may be
produced by a bacterial, yeast or mammalian expression system.
(Updated on 25-MAR-2003 to correct PA field.)
                                                  chimeric mouse human antibodies - used in treatment, diagnosis prophylaxis of HIV infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Light (kappa) chain variable region of murine 1C11 immunoglobulin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New chimeric mouse-human antibodies - used to detect, kill and remove HIV-1 antigen from sample
                                                                                                                                                                                                                     89.3%; Score 590; DB 12; Length 126; 89.7%; Pred. No. 3.7e-38; ive 7; Mismatches 6; Indels (
 Robinson RR
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Ghoshdasti P,
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                                                                                      Disclosure; Fig 13; 108pp; English
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(first entry)
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Better MD, Horwitz AH,
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                    WPI; 1991-178106/24
                                                                                                                                                                                                                                                                                                                                                                             GTKLEI 126
                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                 126 AA;
                                N-PSDB; AAQ12017
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15-AUG-1991
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                  monoclonal antibody (MAb), ICII, and is specific for an HIV-1
viral antigen. It is used in the construction of a chimeric
Mab comprising heavy and light chains having murine V regions
and human C regions. The chimeric Mabs are more effective than
murine MAb ICII since they have an increased compatibility in
humans. The heavy and light chain V-regions are joined by
manipulating their respective joining (J) regions, to generate
restriction enzyme recognition sites. The chimeric MAbs can be
used as immunoconjugates, in association with e.g. toxins for HIV
treatment. They can also be used in diagnosis of HIV.
C Updated on 25-MAR-2003 to correct PI field.)
(Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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This is the light (kappa)- chain variable (V) region of a mous monoclonal antibody (MAb), 1C11, and is specific for an HIV-1
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Pred. No. 3.7e-38;
7; Mismatches 6; Indels
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Best Local Similarity 89.7
Matches 113; Conservative
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Compugen Ltd.
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GenCore version (c) 1993 - 2003
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Listing first 45 summaries
                          - protein search, using sw model
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661
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Match Length DB
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interaction precursor V region (M-T151) - mouse (fragment)
C, Species: Mus musculus (house mouse)
C, State Stat

122 TKLEIN 127 |||||| 121 TKLEIN 126

g 6

90 90 90 90

10 479 72.5 1111 2 E38740 Ig kappa chain V r	C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;35-109/Domain: immunoglobulin homology <imm></imm>	C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;35-109/Domain: immunoglobulin homology <imm></imm>	Query Match 95.6%; Score 632; DB 2; Length 126; Best Local Similarity 93.7%; Pred. No. 2.36-48; Matches 118; Conservative 8; Mismatches 0; Indels 0; Gaps	AQFLGLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLWW 	•
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A;Residues: 1-115 <KAA>
A;Residues: 1-115 <KAA>
A;Residues: L-115 <KAA>
A;Cross-references: GB:M27793; NID:g197161; PIDN:AAA38937.1; PID:g197162
A;Note: the authors translated the codon AGG for residue 30 as Ser
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
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                                                                       Length 122,
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Pred. No. 3.3e-44;
4; Mismatches 0; Indels
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                                                                           Score 607; DB 2;
Pred. No. 3.4e-46;
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Pred. No. 9e-44;
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                                                                                                                                                   6; Mismatches
   F;30-104/Domain: immunoglobulin homology <IMM>
                                                                       91.8%;
95.0%;
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Matches 111; Conservative
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                                                                               Query Match
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C;Accession: A26406
R;Sanz, 1.; Capra, J.D.
Proc. Natl. Acad. Sci. U.S.A. 84, 1085-1089, 1987
A;Title: V-K and J-K gene segments of A/J Ars-A antibodies: somatic recombination genera
A;Acfestence number: A26406
A;Molecule type: DNA
A;Residues: 1-128 <SAN>
A;Residues: 1-128 <SAN>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin homology <IMM>
C;Superfamily: immunoglobulin homology <IMM>
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Grapcies: Mus musculus (house mouse)
Grapcies: Mus musculus (house mouse)
Graces: Musculus (house mouse)
Graces: Musculus (house)
Graces: Musculu
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Date: 30-Jun-1989 #sequence_revision 30-Jun-1991 #text_change 21-Jan-2000
Accession: A26406
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F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-127/Product: Ig light chain V region #status predicted <WAT>
F;36-110/Domain: immunoglobulin homology <IMM>
                                                                                                                                                       Length 127;
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Pred. No. 9.7e-48;
                                                                                                                                               Score 627; DB 2;
Pred. No. 6.4e-48;
6; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             kappa chain V region (Ars-A) - mouse
                                                                                                                                               94.9%;
ilarity 93.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 94.6%; sl Similarity 93.7%; 118; Conservative
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Best Local Similarity
Matches 118; Conserv
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Best Local Similarity
Matches 118; Conserv
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C;Accession: A01927
R;Siegelman, M.; Capra, J.D.
Proc. Natl. Acad. Sci. U.S.A. 78, 7679-7683, 1981
A;Title: Complete amino acid sequence of light chain variable regions derived from five 1, A;Reference number: A01927; MUD:82150934; PMID:6801658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapi hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lar C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Molecule type: protein
A,Residues: 1-108 <SIE>
A,Experimental source: strain A/J
A,Note: HP 93G7 differs in having 93-Met; HP 123E6 differs in having 7-Ser, 92-Tyr, and Arg, 84-Ser, and 93-Ala
C;Comment: The sequence shown is HP R16.7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig kappa chain V regions (anti-arsonate hybridoma proteins) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jul-1982 #sequence_revision 06-Jul-1982 #text_change 21-Jan-2000
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                                                                                                                NID: 9511039; PIDN: CAA38889.1; PID: 9511040
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A,Residues: 1-107 <MEE>
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: hereroterramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                        A;Cross-references: EMBL:X55049; NID:9511039; PIDN:CAA38889.1; C;Superfamily: immunoglobulin V region; immunoglobulin homology F;16-90/Domain: immunoglobulin homology <IMM>
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81.4%; Score 538; DB 2; L
Best Local Similarity 96.2%; Pred. No. 3.2e-40;
Matches 102; Conservative 4; Mismatches 0;
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ilarity 95.3%; Pred. No. 1.6e-39;
Conservative 4; Mismatches 1;
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    A;Status: preliminary; translation not shown
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 14-Feb-1997 Hacquence revision 13-Mar-1997 #text_change 21-Jan-2000
C;Accession: $69900; $69907; $59908
R;Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.
Immunology 75, 116-121, 1992
A;Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin
A;Reference number: $69900; MUID:92165291; PMID:1537587
A;Attle: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin
A;Reference number: $69900; MUID:92165291; PMID:1537587
A;Accession: $69900
A;Seatus: preliminary; translation not shown
A;Molecule type: DNA
A;Accession: $69907
A;Accession: $69907
A;Accession: $69908
A;Accession: $69908
A;Accession: $69908
A;Accession: $69908
A;Accession: $69908
A;Accession: $69908
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569903
Ig Ampa chain (clone KL2.29 / KL2.33 / KL3.8) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C;Accession: 569904; 569904
R,Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.
Immunology 75, 116-121, 1992
Immunology 75, 116-121, 1992
Immunology 75, 116-121, 1992
A;Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin A;Reference number: 569903
A;Accession: 569903
A;Accession: 569903
A;Accession: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-108 <WyS>
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                                                                            PQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKPDGTIKLLIYYTSRL
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A;Residues: 1-108 <WY3.>
A;Residues: 1-108 <WY3.>
A;Cross-references: EMBL:X55046, NID:g511033, PIDN:CAA38886.1; PID:g511034
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>
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    0; Indels
    3; Mismatches
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103; Conservative
109; Conservative
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                                                                                                                                                                                                                                                                                                                                                                            Species: Mus musculus (house mouse)
.Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
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R; Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P. submitted to the EMBL Data Library, March 1992
A; Description: Structural characterization of CD4 mAb.
A; Reference number: S19963
A; Accession: S19970
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-108 < WEI>A; Accession: S19970
C; Superfemence: EMBL:X65095; NID:952286; PIDN:CAA46223.1; PID:9
C; Superfement; immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 16-90/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                         61 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPRTFGGGTKLEI 106
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R. Meek, K.; Sanz, I.; Rathbun, G.; Nisonoff, A.; Capra, J.D.
Proc. Natl. Acad. Sci. U.S.A. 84, 6244-6248, 1987
A.Title: Identity of the V-kappa-10-Ars-A gene segments of the A-Title: Identity of the V-kappa-10-Ars-A gene segments of the A-Accession: A28044
A. McCession: A28044
A. Mollo: B7317629; PMID: 3114744
A. Mesidues: 1-107 AME>
C. Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>
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Pred. No. 2.9e-39;
5; Mismatches 2; Indels
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80.0%; Score 529; DB 2;
Best Local Similarity 95.3%; Pred. No. 1.9e-39;
Matches 101; Conservative 2; Mismatches 3;
                    Score 529; DB 2;
Pred. No. 1.9e-39;
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C;Species: Mus musculus (house mouse)
                                                                3; Mismatches
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                    80.0%;
95.3%;
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Best Local Similarity 93.4%;
Matches 99; Conservative
                  Query Match
Best Local Similarity 95.3'
Matches 101; Conservative
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R;Shalaby, M.R.; Shepard, H.M.; Presta, L.; Rodrigues, M.L.; Beverley, P.C.L.; Feldmann, D. Exp. Med. 175, 217-225, 1992
A;Title: Development of humanized bispecific antibodies reactive with cytotoxic lymphocy A;Reference number: PH0885; MUID:92113462; PMID:1346155
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Ig kappa chain (clone KL2.28) - mouse C; Species: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Date: 14-Peb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000 C; Accession: S69902 R; Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C. Immunology 75, 116-121, 1992 A; Title: B-cell proliferation initiated by Ia cross-linking and sustained by A; Reference number: S69900; MUID:92165291; PMID:1537587
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C;Species: Was musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession: S38862
R;Fischer, R; Voss, A:, Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.
Ribantted to the EMBL Data Library, August 1993
A;Description: Production and cloning of TMV-specific monoclonal antibodies.
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C;Species: Mus musculus (house mouse)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;Ie-90/Domain: immunoglobulin homology <IMM>
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Pred. No. 2.9e-39;
4; Mismatches 2; Indels
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Matches 100, Conservative
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us-09-114-285a-29.rpr

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21 DIOMIQITSSLSASLCDRVIISCRASODISSYLNWYQQRPDGTIKLLIYYTSRLHSGVPS 80
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A,Reference number: S37200
A,Accession: S3862
A,Status: preliminary
A,Rolecule type: mRNA
A,Residues: 1-108 <FIS>
A,Cross_references: EMBL:X75854; NID:6429109; PID:g429110
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Reywords: heterocteramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
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A Siegelaman M., Capra J.D.;

Siegelaman M., Capra J.D.;

Complete amino acid sequence of light chain variable regions derived

from five monoclonal anti-p-azophanylarsonate antibodies differing

with respect to a crossreactive idiotype.";

L. With respect to a crossreactive idiotype.";

Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).

-! MSCELIANBOUS ANTI-ARSONATE HYBRIDOMA PROTEIN.

PIR, A01927; KNWSAR.

RISSP, P01607; IREI.

InterPro; IPR001106; Ig-like.

InterPro; IPR001006; Ig-MHC.

R InterPro; IPR001006; Ig-MHC.

R SMART; SM00406; IGV; I.

R SMART; SM00406; IGV; I.

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 530; DB 1;
Pred. No. 2.6e-46;
                                                                                                                                                                                                 KVSK MOUSE STANDARD; PRT; 108 AA. P01644; 21-JUL-1986 (Rel. 01, Created) 21-JUB (Rel. 01, Last sequence update) 21-JUB FEB-2003 (Rel. 41, Last annotation update) 19 kappa chain V-V region HP R16.7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAMEWORK-1
         KV31 MOUSE
KV50 MOUSE
KV5B MOUSE
KV3M MOUSE
KV30 MOUSE
KV4B HUMAN
                                                                       KV1C_HUMAN
KV1K_HUMAN
                                                                                            KV5T MOUSE
                                                                                                                                                                                                                                                                                                                               STRAIN=A/J;
MEDLINE=82150934; PubMed=6801658;
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ilarity 95.3%;
Conservative
                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
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35
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108
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Best Local Simi:
Matches 101; (
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Matches 100;
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P01646;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                    Siggelman M., Capra J.D.;

"Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsonate antibodies differing with respect to a crossreactive idiotype.";

Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683 (1981).

-! MISCELLANBROUS: ANTI-ARSONATE HYBRIDOWA PROTEIN.

HSSP; PO1607; 1REI.

InterPro; IPR003106; Ig_MHC.

InterPro; IPR00356; Ig_V.

Ffam; PP00047; ig; 1.

SWART; SM00406; IGV; 1.

PROSITE; PSS0835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-82150934; PubMed-6801658; Siegelman M., Capra J.D.; Capelman M., Capra J.D.; "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophanylarsonate antibodies differing with respect to a crossreactive idiotype.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS
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                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
VCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                               COMPLEMENTARITY - DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                  COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                       79.9%; Score 528; DB 1; Length lux
95.3%; Pred. No. 4.2e-46;
without 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNMLPRTFGGGTKLEI
                                                                                                                                                                                                                                                                                                                                                                                                11954 MW; 22F4642C63EFF58E CRC64;
                             (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 41, Last annotation update)
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21-JUL-1986 (Rel. 01, Last sequence update)
28-FBS-2003 (Rel. 41, Last annotation update)
Mus musculus (Mouse)
         108 AA
                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                              FRAMEWORK-3.
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                                                           Ig kappa chain V-V region HP 93G7.
Mus musculus (Mouse).
                                                                                                                                    STRAIN=A/J;
MEDLINE=82150934; PubMed=6801658;
                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 95.3
Matches 101; Conservative
        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                108 AA;
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                              21-JUL-1986
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                                                  28-FEB-2003
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         KVSL MOUSE
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SEQUENCE
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"Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsonate antibodies differing with respect to a crossreactive idiotype.";

Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683 (1981).

-!- MISCELLANBOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.

INTERPRO; IPR007110; Ig-like.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003096; Ig_W.

Pfam; PF00447; ig; 1.

SMART; SM04406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DIOMIQITSSLSASLGDRVIISCRASQDINNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 DIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKPDGTIKLLIYYTSRLHSGVPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Pred. No. 8.3e-46;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 RFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGGGTKLEI 126
                                                                                                                                                                                                                                                             FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                         COMPLEMENTARITY - DETERMINING - 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11965 MW; 39971BC653EFEFA2 CRC64;
Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
-!- MISCELLANBOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
HSSP; PO1667; IREI.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-EBB-2003 (Rel. 41, Last annotation update)
1g kappa chain V-V region HP 123E6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY
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                                                                                                                                                   PERMY PF00047; ig; 1.
SMART, SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.48;
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Conservative
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Matches

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropen Bioinformatics Institute of The are are trictions on its use by non-profit institutions as long as its content is in no way
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noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 DIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKPDGTIKLLIYYTSRLHSGVPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIOMIQITSSLSASLGHRVTITCSASODISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                   MEDLINE=83271467; PubMed=6877353;
Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
"mRNA sequences define an unusually restricted IgG response to.
Phenyloxazolone and its early diversification.";
Nature 304:320-324 (1983).
-!- MISCELLANBOUS: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 RFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGGGTKLEI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPLEMENTARITY - DETERMINING - 1.
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COMPLEMENTARITY-DETERMINING-3.
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Pred. No. 3.3e-43;
....rrhes 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 kappa chain V-V region MOPC 173.
Mus musculus (Mouse).
13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
12-UUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-V region NQS-89.4
                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See h or send an email to license@isb-sib.ch).
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BY SIMILARITY
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SMART; SMO0406; 167; 1.
PROSTITE; PSS0835; IG LIKE; 1.
Immunoglobulin V region; Hybridoma.
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SEQUENCE.
MEDLINE=76091934; PubMed=812696;
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfan; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
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89.6%;
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88
97
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88
                                                                              Mus musculus (Mouse)
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108 AA;
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nes 95; Conserv
                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                               NCBI_TaxID=10090;
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Complete amino acid sequence of light chain variable regions derived

T "Complete amino acid sequence of light chain variable regions derived

from five monoclonal anti-p-azophenylarsonate antibodies differing

trom five monoclonal anti-p-azophenylarsonate antibodies differing

L Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).

- I- MISCELLANBOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.

R HSSP, PO1667; ANTI-ARSONATE HYBRIDOMA PROTEIN.

R InterPro; IPR007110; Ig-like.

R InterPro; IPR007110; Ig-like.

R InterPro; IPR003596; Ig_V.

R Pfam; PF00047; Ig. 1.

R RMART; SM04406; IGV; 1.

R PROSITE; PS50835; IG LIKE; 1.

M Immunoglobulin V region.

T DOMAIN
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                                                                                                                                   DIOMIQTPSSLSASLGDRVIISCRASQDINNYLNWYRQKPDGTVKLLIYYTSRLHSGVPS 60
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                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                             Mus mūsculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 RFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGGGTKLEI 126
                                        Length 108;
                                                                                                                                                                                      81 RFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGGGTKLEI 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPLEMENTARITY-DETERMINING-3
                   77.6%; Score 513; DB 1; Length 10: 91.5%; Pred. No. 1.3e-44; ive 6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11961 MW; D52EDA5E9A45291C CRC64;
   108 AA; 11989 MW; 4C98599C08EBA09A CRC64;
                                                                                                                                                                                                                                                                                                                                                     21.JUL-1986 (Rel. 01, Created)
21.JUL-1986 (Rel. 01, Last sequence update)
21.FEB-2003 (Rel. 41, Last annotation update)
Ig kappa chain V-V region HP 91A3.
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MEDLINE=82150934; Pubmed=6801658;
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Best Local Similarity 91.5'
Matches 97; Conservative
                                                                            99; Conservative
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108 1
108 AA;
                                      Query Match
Best Local Similarity
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ID KVSU MOUSE
AC P04946;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 DIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKPDGTIKLLIYYTSRLHSGVPS
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Seidman J.G., Max E.E., Leder P.;
"A Kappa-immnoglobulin gene is formed by site-specific recombination
without further somatic mutation.";
Nature 280:370-375(1979).
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                     "Determination of the primary structure of a mouse IgG2a minuroglobulin. Amino-acid sequence of the light chain."; Eur. J. Biochem. 59:525-537(1975).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 23-130, MEDLINE=67056897; PubMed=4162931; Gray W.R., Dreyer W.J., Hood L.; "Mechanism of antibody synthesis: size differences between mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 155:465-467 (1967).
-!- MISCELLANEOUS: THIS PRECURSOR WAS SYNTHESIZED IN A CELL-FREE
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FRAMEWORK-3.
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COMPLEMENTARITY-DETERMINING-1.
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83.0%; Pred. No. 1.3e-40;
iive 10; Mismatches 8;
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21-UUL-1986 (Rel. Ol, Created)
21-UUL-1986 (Rel. Ol, Last sequence update)
21-UL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-V region MOPC 41 precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAMEWORK-2
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                                                                                                                                                                                                                                                                              Pfam; PF00047; 1g; 1. SMART; SM00406; 1Gv; 1. PROSITE; PS50835; 1G_LIKE; 1.
                                                                                                                                                                 HSSP; PO1607; IREI.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
Fougereau M.;
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HSSP; P01607; 1REI.
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Best Local Similarity
Matches 88; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 MRAPAQI FGFULLLFQCTRCDIQMTQSPSSLSASLGERVSLTCRASQDIGSSLNWLQQEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                        IG KAPPA CHAIN V-V REGION MOPC 41.
RAMBWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
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MISSING (IN 25% OF THE MOLECULES)
SYSTEM DIRECTED BY MRNA ISOLATED FROM MYELOMA POLYSOMES-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
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COMPLEMENTARITY-DETERMINING-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14311 MW; SEFEOFE71D5F1BEC CRC64;
                                                  PIR; A93211; KVMSM4.

HSSP; P01607; 1REI.

InterPro; IPR007110; Ig-like.

InterPro; IPR003596; Ig MHC.

InterPro; IPR003596; Ig_v.

Pfam; PR00047; 1g; 1.

SMART; SM00406; IGv; 1.

Immunoglobulin V region; Signal; Bence-Jones protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68.2%; Score 451; DB 1;
70.6%; Pred. No. 2.6e-38;
iive 13; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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Homo sapiens (Human).
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PIR; A01883; KIHUWK.
HSSP; P01607; 1REI.
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InterPro; IPR003596; Ig_v.
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SEQUENCE
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KV11_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=81052342; PubMed=6776411;
Altenburger W., Steinmetz M., Zachau H.G.;
"Functional and non-functional joining in immunoglobulin light chain
genes of a mouse myeloma.";
Nature 287:603-607(1980)
                                                                                                                                                                                                                                                              Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
NCBI_TaxID=10090;
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0
                                                                                                               IG KAPPA CHAIN V-I REGION WALKER.
                                                                                                                                                                                                                                         Length 129;
                                                                                                                                   COMPLEMENTARITY-DETERMINING-1.
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                                                                                                                                                                            COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                                                             23; Indels
                                                                                                                                                                                                                     14069 MW; F941FA07D4AFC2F9 CRC64;
        GO; GO:0003823; F:antigen binding activity; NAS. GO; GO:0006955; P:immune response; NAS. InterPro; IPR007110; Ig-like. InterPro; IPR003066; Ig-MHC. InterPro; IPR003596; Ig-V.
                                                                                                                                                                                                                                        65.2%; Score 431; DB 1; 70.5%; Pred. No. 2.6e-36; iive 13; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-V region T1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                         128 AA
                                                                                                                                                                                                BY SIMILARITY
                                                                                                                                               FRAMEWORK-2.
                                                                                                                                                                   FRAMEWORK-3
                                                                                                                                                                                       FRAMEWORK-4
  GO:0005576; C:extracellular; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                       SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
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InterPro, IPR007110, Ig-like.
InterPro, IPR003006, Ig_MHC.
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56
71
                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                           Pfam; PF00047; ig;
SMART; SM00406; IGv
PROSITE; PS50835; I
                                                                                                                                                                                                                    129 AA;
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EI 128
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DGTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MRTPAQFLGILLLWFPGIKCDIKWTQSPSSWYASLGERVTISCKASQDINSYLTWFQQKP 60
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"Human immunoglobulin variable region genes -- DNA sequences of two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                           IG KAPPA CHAIN V-V REGION TI.
PRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
PRAMEWORK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 128;
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                                                                                                                                                                                                                                                            FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                         62.9%; Score 416; DB 1; Length 12 ilarity 63.5%; Pred. No. 8.1e-35; Conservative 20; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                           14385 MW; AFA5563D31BB7E05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 13, Last annotation update)
15-JUL-1999 (Rel. 13, Last annotation (Fragment).
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                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
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MEDLINE=83129397; PubMed=6402305;
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Pfam, PF00047; ig; i. "-
SMARY; SM00406; IGv. i. "-
PROSITE, PS50835; IG LIKE; i.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kappa genes and a pseudogene.";
Nature 288:730-733(1980).
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nes 80; Conserv
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Immunoglobulin V
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KV10 HUMAN
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MEDLINE=77250895; PubMed=70482;

A Capra J.D., Tung A.S., Nisonoff A.;

Capra J.D., Tung A.S., Nisonoff A.;

Capra J.D., Tung A.S., Nisonoff A.;

Structural studies on induced antibodies with defined idiotypic

T specificities. V. The complete amino acid sequence of the light chain

variable regions of anti-p-azophenylarsonate antibodies from A/J mice

T specificities. V. The complete amino acid sequence of the light chain

variable regions of anti-p-azophenylarsonate antibodies from A/J mice

L J. Immunol. 119:993-999(1977).

C J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 AQFLGLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKPDGTI
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 KLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLP 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.3%; Score 412; DB 1; Length 117; 72.1%; Pred. No. 1.8e-34; ive 12; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                    IG KAPPA CHAIN V-I REGION HK10 FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Ig kappa chain V-V regions (Anti-arsonate antibodies).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12799 MW; D7D0FF3718CEF587 CRC64;
                                                      GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006855; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_NHC.
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                                                                                                                                                                                        PEam; PF00047; ig; 1. SMART; SM00406; IGv; 1. PROSITE; PS50835; IG LIKE; 1. Immunoglobulin V region; Signal.
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InterPro; IPR003006; 19_MHC.
InterPro; IPR003596; 19_V.
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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Best Local Similarity 72.1%
Matches 80; Conservative
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56
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               PIR; A01881; K1HU11.
HSSP; P01607; IREI.
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Palm M., Hilschmann N.;
Palm M., Hilschmann N.;
The primary structure of a crystalline monoclonal immunoglobulin
"The primary structure of a crystalline spote of the structure of acrystalline monoclonal immunoglobulin
and characterization of the tryptic peptides; the complete amino acid
sequence of the protein; a contribution to the elucidation of the
three-dimensional structure of antibodies, in particular their
combining site.";
Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
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MEDLINE=76039968; PubMed=1182131;
Epp O., Lattman B.E., Schiffer M., Huber R., Palm W.;
"The molecular structure of a dimer composed of the variable portions of the Bence-Jones protein REI refined at 2.0-A resolution.";
Biochemistry 14:4943-4952(1975).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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GO: GO: 0003823; F:antigen binding activity; NAS.
GO: GO: 0003823; F:antigen binding activity; NAS.
GO: GO: 000595; P:immune response; NAS.
InterPro; IPR003106; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Fam: PP00047; ig_1 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Bence-Jones protein; 3D-structure.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                  81 RESGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGGGTKLEI 126
                                 FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                         61.4%; Score 406; DB 1; Length 108; 74.5%; Pred. No. 6.7e-34; Live 10; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                      61 RFSGSGSGTDFTLTIDPMEEDDTATYFCQQSRLIPRTFGGGTKLEI 106
                 COMPLEMENTARITY - DETERMINING-1.
                                                                       FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                        12056 MW; AE2861E6AAC09DD2 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
18 Kappa chain V-I region Rei
Homo sapiens (Human)
                                                                                                              FRAMEWORK-4.
BY SIMILARITY
FRAMEWORK-1
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 PIR; A91663; KIHURE.
PDB; IREI; 17-FEB-84.
PDB; IAR2; 12-NOV-97.
PDB; IBWW; 29-DEC-99.
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65 KLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGGGTKL
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Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
Solomon A., Stevens F.J., Schiffer M.;
"Comparison of crystal structures of two homologous proteins:
structural origin of altered domain interactions in immunoglobulin
light-chain dimers.";
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MEDLINE-81267384; PubMed=6167731;
Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
Stevens F.J., Solomon A.;
"Characterization and preliminary crystallographic data on the VL-related fragment of the human kI Bence Jones protein Wat.";
J. Mol. Biol. 147:185-193 (1981).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                         KAPPA CHAIN V-I REGION DAUDI
                                                                                                                                                                                                                                       IG KAPPA CHAIN V-I REGION DAUD
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 129;
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FRAMEWORK-4.
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62.8%; Pred. No. 3.3e-33;
Mismatches 26; Indels
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SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS)
                GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0005955; P:ammune response; NAS.
InterPro: IPR00110; IQ-like.
InterPro: IPR00110; IQ-V.
InterPro: IPR003596; IQ-V.
Ffam; PF00047; IG':
SMART; SM00406; IG':
Immunoglobulin V region; Signal.
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
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01-NOV-1995 (Rel. 32, Last sequence update)
01-RDS-2003 (Rel. 41, Last annotation update)
1g kappa chain V-I region WAT.
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  GO:0005576; C:extracellular; NAS.
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es 76; Conserv
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P80362;
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KV1Y HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
  DOR NO DO
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MEDLINE=85014148; PubMed=6091049;
MEDLINE=85014148; PubMed=6091049;
Midbeck H.G., Combriato G., Zachau H.G.;
"Immunoglobulin genes of the kappa light chain type from two human lymphoid cell lines are closely related.";
Nucleic Acids Res. 12:6995-7006(1984).
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 108;
COMPLEMENTARITY-DETERMINING-1.
                                                                                  COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.5%; Score 400; DB 1; Length 1072.6%; Pred. No. 2.7e-33; ive 12; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11902 MW; 9E8143E1188BCE2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G kappa chain V-I region Daudi precursor.
Homo sapiens (Human)
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                                                                FRAMEWORK-3.
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Best Local Similarity 72.00
To 77; Conservative
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KV1X HU P04432;

KV1X_HUMAN

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R GO; GO:0006955; P:immune response; NAS.
R InterPro; IPR00110; Ig-like.
R InterPro; IPR003006; Ig_MHC.
R InterPro; IPR003006; Ig_MHC.
R SMART; SMO0406; Ig_V.
R PROSITE; PS50835; Ig_Like; 1.
DOMAIN 24 FRAMEWORK-1.
T DOMAIN 35 6 COMPLEMENTARITY-DETERMINING-1.
T DOMAIN 57 86 FRAMEWORK-3.
T DOMAIN 57 88 COMPLEMENTARITY-DETERMINING-2.
T DOMAIN 99 107 FRAMEWORK-3.
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T DOMAIN 98 107 FRAMEWORK-4.
T CONFLICT 30 31 TN -> SD (IN REF. 2).
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11737 MW; D9D941B3F0FAE697 CRC64;
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1 DIQMTQSPSSLSASVGDRVTITCRASQDITNYVNWFQQRPGQAPKVLIYGASILETGVPS 60 g ò g

21 DIOMIOTISSLSASLGDRVTISCRASQDISSYLNWYQQKPDGTIKLLIYYTSRLHSGVPS 80

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Gaps .; 0

Search completed: October 22, 2003, 22:17:09 Job time : 13.9886 secs

Q8K1f3 mus musculu Q8K1f1 mus musculu Q8K1f1 mus musculu Q9Gyf0 mus musculu Q9Gyf0 mus musculu Q9Gyf0 mus musculu Q8K1f2 mus musculu Q8K0f8 mus musculu Q9Cob mus musculu Q9L178 homo sapien Q9L18 homo sapien Q9L18 homo sapien Q9L18 mus musculu Q9L18 homo sapien Q9L16 mus musculu Q9L18 homo sapien Q9L16 mus musculu Q9L18 homo sapien Q9L16 mus musculu Q9L18 mus musculu Q9L18 mus musculu Q9L18 mus musculu Q9L18 mus musculu Q9L12 mus musculu Q9L

Seguence:

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1 MVSSAQFLGLLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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TISSUB-Colon;
Strausberg R.;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
1-DEC-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 25-9 kDa protein.
Mus musculus (Mouse).
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08K1F2
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08K0F6
08K0F8
09K0F8
09K0F8
09UL78
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                                                                                                                                                                                       October 22, 2003, 22:13:15 ; Search time 58.2083 Seconds
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1 MVSSAQFLGLLLCFQGTRC.......CQQGNTLPYTFGGGTKLEIN 127
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Maximum Match 100%
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Maximum DB seq length: 200000000
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EMBL; AF124721; AAK55120.1; -...
InterPro; IPR007110; Ig-like.
InterPro; IPR00306; Ig MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG MHC; 1.
Hypothetical protein.
NON TER 1 1
SEQÜENCE 233 AA; 25781 MW;
                                                                                              Best Local Similarity, 87.17
Matches 101; Conservative
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                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
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SEQUENCE
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                                                                                                                  01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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86.8%; Score 574; DB 11; Length 234;
Best Local Similarity 87.3%; Pred. No. 5.8e-54;
Matches 110; Conservative 7; Mismatches 9; Indels (
                                                                                                                                                                                                                                   N 14.1

P SEQUENCE FROM N.A.

C TISSUE-Colon;

A Straueberg R.;

Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

L Submitted (APR-2002) to 19-1ike.

R InterPro; IPR003106; Ig-NHC.

R InterPro; IPR003306; Ig-NHC.

R InterPro; IPR003306; Ig-V.

R Ffam; PF00047; ig; 2.

SMART; SM00406; IGV; 1.

P ROSITE; PSS00835; IG_LIKE; 2.

R PROSITE; PSS00835; IG_LIKE; 2.

R PROSITE; PSS00805; IG MHC; 1.

Hypothetical protein.

W Hypothetical protein.
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TISSUB-COlon;
Straubberg R.,
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013496; AAH13496.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 25,8 kba protein (Fragment).
Mus musculus (Mouse).
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                                                                                                  PRELIMINARY;
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           GTKLEI 126
                                    121 GTKLEV 126
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61 DGTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGG 120
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                                                                                                                                                                     11 LLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKPDGTIKLLIYY
                                                                                                                                                                                                                                                                                   71 TSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGGGTKLEI 126
                                                                                                                                                                                                                                                                                                                70 TSSLHSGVPSRPSGSGSGTDYSLTISNLEPEDIATYXCQQYRYLPWTFGGGTKLEI 125
                                                                                                                 Gaps
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MEDLINE=99306687; PubMed=10380019;
Tripathi P.K., Qin H., Bhattacharya-Chatterjee M., Ceriani R.L.,
Tripathi P.K., Chatterjee S.K.;
"Construction and characterization of a chimeric fusion protein
construction and characterization of a chimeric fusion protein
associated antigen and the cytokine GM-CSF.";
Hybridoma 18:193-202(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
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                                                         Length 233;
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127 AA; 13794 MW; 13F61BEBBB981FAS CRC64;
233 AA; 25781 MW; BIC184DA149A16EB CRC64;
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Last annotation update)
                                                         80.8%; Score 534; DB 11;
87.1%; Pred. No. 1.2e-49;
iive 7; Mismatches 8;
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01-DEC-2001 (TrEMBLrel. 19, Last sequen
01-MAR-2003 (TrEMBLrel. 23, Last annote
Immunoglobulin light chain (Fragment).
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Query Match
Best Local Similarity
Matches 80; Conserv
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      SEQUENCE
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09UL77;
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Q9UL77
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
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"Molecular analysis of polyreactive monoclonal antibodies from
rheumatric carditis: human anti-N-acetylglucosamine/anti-myosin
antibody V region genes.";
J. Immunol. 161:2020-2031(1998).
                                                                                                                                                                                                                                                                                                                                             STRAIN-BALB/c;
MEDLINE=20448942; PubMed=10992488;
Malkiel S., Liao L., Cunningham M.W., Diamond B.;
T-Cell-dependent antibody response to the dominant epitope of streptococcal polysoccharide, N-acetyl-glucosamine, is cross-rewith cardiac myosin.";
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Anti-myosin immunoglobulin light chain variable region
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EMBL; AP206022; AAF69320.1; --
HSSP; P80362; IMTL.
INTERPO; IPR003106; Ig-like.
INTERPO; IPR003006; Ig_MHC.
INTERPO; IPR003506; Ig_V.
Fam; PF0047; ig; 1.
SMART; SM0406; IGV; 1.
PR081TE; PS50835; IG_LIKE; 1.
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InterPro: IPR007110; Ig-11ke.
InterPro: IPR003006, Ig_MHC.
InterPro: IPR003006, Ig_WHC.
Ffam; PF00047; ig; 1.
SMART; SM0406, IGv; 1.
NON TER 107 107
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                                                                                                                                                                           21 DIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKPDGTIKLLIYYTSRLHSGVPS 80
                                                                                                                                                                                                          1 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 DIOMIQITSSLSASLGDRVIISCRASQDISSYLNWYQQKPDGTIKLLIYYTSRLHSGVPS
                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                    Length 107;
                                                                                                                                                                                                                                                                                                                                 81 RFSGSGSGTDYSLTINNLEQEDIATYFCQQG-NTLPYTFGGGTKLEI 126
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MabLinEs-98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 59.0%; Score 390; DB 4; Length 108; Best Local Similarity 71.7%; Pred. No. 1.7e-34; Matches 76; Conservative 12; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 RFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGGGTKLEI 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                 13; Indels
107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 AA; 11738 MW; C06681716C4D16F3 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 25.7 kBa protein.
Mus musculus (Mouse).
                                                       DB 4;
                                                       59.4%; Score 392.5; DB 4 ilarity 74.8%; Pred. No. 9.1e-35; Conservative 11; Mismatches 13
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Clin. Immunol. Immunopathol. 87:184-192(1998)
BMBL; AF035037; AAD56273.1; -.
INSEP: PO1667; IRBI.
InterPro; IPR007110; Ig-like.
InterPro; IPR00306; Ig_MHC.
InterPro; IPR003596; Ig_W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam, PF00047, ig, 1.
SMART, SM00406, IGv, 1.
PROSITE, PS50835, IG_LIKE, 1.
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61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPRTFGPGTKLEI 106
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Kappa light chain of Mab7 (Fragment)
Mus musculus (Mouse).
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PROSITE; PS50835; IG_LIKE; 1.
NON TEP
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les 74; Conserv
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ID Q9R1A5
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                         6 QFLGLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKPDGTIK
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'Myosin-reactive autoantibodies in rheumatic carditis and normal
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58.9%; Score 389; DB 11; Length 234;
Best Local Similarity 61.2%; Pred. No. 6.1e-34;
Matches 74; Conservative 19; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. WEDDMed=9614934; WEDLINE=98277139; PubMed=9614934; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 108;
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                                         TISSUE-Colon;
Straubberg R.;
Submitted (BCC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC019474; AAH1944.1; -..
InterPro; IPR03006; Ig_MHC.
InterPro; IPR03366; Ig_V.
Pfan; PF00047; ig; 2.
SMART; SM00406; IGV.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                       al protein.
234 AA; 25702 MW; 102551C58AC2FA9F CRC64;
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EMBL; AF035044; AAD56280.1; -.
HSSP; PO1607; IREI.
InterPro; IPR007110; Ig-like.
InterPro; IPR00306; Ig_MHC.
InterPro; IPR003996; Ig_V.
Pfan; PF0047; ig; 1.
SMART; SM00406; IGV.
NOW.
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Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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108 AA;
                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                         Hypothetical
SEQUENCE 23
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NON TER
SEQUENCE
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Q9UL70
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Milde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
"Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
antibody (Mab 7, its light and heavy chains) and construction of a
single chain antibody (ScFV).";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF152311, AAD40242.1; -.
HSSP; PO1679; 2FBJ.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003006; Ig_MHC.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDINE-98277139; PubMed=9614934; MEDLINE-98277139; PubMed=9614934; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., · · Young D.C.; "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56.1%; Score 370.5; DB 4; Length 107; 69.8%; Pred. No. 2.2e-32; ive 12; Mismatches 19; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 RFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGGGTKLEI 126
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 AA; 11501 MW; 070549FDE0754748 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ciin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035033, AAD56269.1; -.
HSSP; PO1607; IREI.
InterPro; IPR003106; Ig-like.
InterPro; IPR003066; Ig_MHC.
InterPro; IPR0030596; Ig_N.
SMART; SM00406; IGV;
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1 DIVLTQSPASLAVSLGQRATISCRASKSVSTSGYSYMHWYQQKPGQPPKLLIYLASNLES 60
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                                                                                                                                                                      Atkin J.D., lape A., Jennings I.G., Horaitis O., Cotton R.G.H.; "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed in Mammalian Cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI TaxID=10090;
                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 GVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGGGTKLEI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 54.9%; Score 363; DB 11; Jength 111; Best Local Similarity 63.6%; Pred. No. 1.5e-31; Matches 70; Conservative 15; Mismatches 21; Indels
                                                                                                                                                                                                                        Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF307935; AAL09419.1; -.
InterPro; IPR007110; IG-11ke.
InterPro; IPR003066; Ig-MHC.
InterPro; IPR003596; Ig-V.
                                                                                                                                                                                                                                                                                                                                                                                                    111 AA; 12046 MW; 1E46988AA6858526 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 AA; 11859 MW; 68506D75613DBFBE CRC64;
01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Pterin-mimicking anti-idiotope kappa chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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STRAIN-C3H/HeJ-lpr/lpr;
MEDLINE=96409289; PubMed=8814271;
                                                                                                                                                                                                                                                                                                             Pfam; PF00047; 1g; 1. SMART; SM00406; 1Gv; 1. PROSITE; PS50835; IG_LIKE; 1.
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PROSITE; PS50835; IG_LIKE; 1.
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Best Local Similarity 60.4%;
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                                                                  Mus musculus (Mouse)
                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                   NCBI_TaxID=10090;
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SMART; SM00406;
                                                      Fragment)
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                                                                                                                                                                                                                                                1 DIQLTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 DIQMIQTISSLSASLGDRVIISCRASQDISSYLNWYQQKPDGTIKLLIYYTSRLHSGVPS 80
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Momo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                    61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPFTFGSGTKLEI 106
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                     55.5%; Score 367; DB 11; Length 2 66.0%; Pred. No. 1.3e-31; tive 17; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB5845F19724FB4E CRC64;
                                                                                                                       214 AA; 23922 MW; 52BA205FDE995E2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clin. Immunol. Immunopathol. 87:184-192 (1998).

EMBL; AF035035; AAD56271.1; -...

HSSP; PO1607; IREE.

InterPro; IRR07110; Ig-like.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_V.

Pfan; PF00047; ig; 1.

SMART; SM00406; IGV; 1.

MANT; PS50835; IG_LIKE; 1.
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Q920E9;
01-DEC-2001 (TrEMBLrel. 19, Created)
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                     Pfam; PF00047; ig; 2.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG_MHC; 1.
InterPro; IPR003596; Ig_v.
                                                                                                                                           Query Match
Best Local Similarity 66.0%
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Best Local Similarity 69.5-
Best A4; Conservative
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SEQUENCE FROM N.A.
MEDLINE=21361171; PubMed=11468171;
COMENDO R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;
COMENDO R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;
The tropism of organ involvement in primary systemic amyloidosis:
Contributions of Ig V(L) germ line gene use and clonal plasma cell
burden.";
Blood 98:714-720(2001).
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                    Query Match 52.6%; Score 348; DB 4; Length 116; Best Local Similarity 62.9%; Pred. No. 6.6e-30; Matches 66; Conservative 20; Mismatches 19; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Kappa 1 light chain variable region (Fragment).
SDNKI.
                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 116 AA.
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Interpro; IPR007110; Ig-like.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
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1096PF6
AC 096PF7
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DT 01-DB6
DT 01-DB6
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Search completed: October 22, 2003, 22:20:15 Job time : 60.2083 secs

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SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
US-08-137-117D-29
Sequence 29, Appl
Sequence 2, Appl
Sequence 2, Appli
Sequence 17, Appl
Sequence 5, Appli
Sequence 37, Appl
Sequence 37, Appl
Sequence 2, Appli
Sequence 2, Appli
                                                                         October 22, 2003, 22:14:35; Search time 13.4697 Seconds (without alignments) 398.931 Million cell updates/sec
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                                                                                                                                              1 MVSSAQFLGLLLCFQGTRC......CQQGNTLPYTFGGGTKLEIN 127
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
          GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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US-08-458-05262-2
US-08-458-100-17
US-08-137-1170-37
US-08-137-1170-37
US-08-574-693A-2
US-09-225-322B-10
US-09-764-304-10
US-09-764-304-10
US-09-364-37-642B-16
US-08-434-37-216
US-08-437-642B-16
US-08-4458-516-9
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                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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661
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Match Length
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107
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Perfect score:
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61 DGTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGG 120
                                                                                                                                                                                                                                                                                                           61 DGTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYFGG 120
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                                                                                                                                                                                                              1 MVSSAQFLGLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
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                                                                                        Length 127;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David
TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH PROMOTE
TITLE OF INVENTION: CENTRAL NERVOUS SYSTEM REMYELINATION
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smithy & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/236,520
FILING DATE: 29-APR-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 27,227
REFERENCE/DOCKET NUMBER: MAV92-01
TELECOMMUNICATION INFORMATION:
                                                                                      100.0%; Score 661; DB 2;
100.0%; Pred. No. 3.8e-61;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 2, Application US/08236520 ; Patent No. 5591629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 617-861-6240
                                                                                                                                         Matches 127; Conservative
                      ; MOLECULE TYPE: protein US-08-436-717-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                           |||||||
121 GTKLEIN 127
                                                                                                                                                                                                                                                                                                                                                                                   121 GTKLEIN 127
linear
                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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                                                                                                                                                                                                                                                                                                              61 DGTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGG 120
                                                                                                                                                                                                                                                                                     61 DGTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGG 120
                                                                                                                                                                                                                1 MVSSAQFLGLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP 60
                                                                                                                                                                                          1 MVSSAQFLGLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
                                                                                                                                            .
0
                                                                                               Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-436-717-29

Sequence 29, Application US/08436717

Sequence 29, Application US/08436717

Patent No. S817790

GENERAL INFORMATION:
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
                                                                                          Query Match
100.0%; Score 661; DB 1;
Best Local Similarity 100.0%; Pred. No. 3.8e-61;
Matches 127; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION NUMBER: UP 4-32084
FILING DATE: 19-PEB-1992
PRIOR APPLICATION NUMBER: UP 3-95476
FILING DATE: 19-PEB-1992
PRIOR APPLICATION NUMBER: UP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY AGENT INFORMATION:
NAME: WEGNET, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (202) 672-5300
(202) 672-5399
                   , MOLECULE TYPE: protein US-08-137-117D-29
                                                                                                                                                                                                                                                                                                                                                                                                                            121 GTKLEIN 127
                                                                                                                                                                                                                                                                                                                                                                                   121 GTKLEIN 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 DGTVKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPWTFGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MMSSAQFLGLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 131;
                                                                                                                                                                                   APPLICANT: Mayor Foundation for Medical Education Research TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH PROMOTE TITLE OF INVENTION: CENTRAL NERVOUS SYSTEM REMYELINATION NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smithy & Reynolds, P.C. STREET: Two Milltia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96.5%; Score 638; DB 5; Length 13:
96.0%; Pred. No. 9.5e-59;
ive 5; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALDGARAL, DELLICIA
NAME: Granhan, Patricia
REGISTRATION NUMBER: 27,227
REFREENCE/DOCKET NUMBER: MMV92-01 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/236,520
FILING DATE: April 29, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                           Sequence 2, Application PC/TUS9505262 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17, Application US/08649100
Patent No. 6114507
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 131 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SHIRAKAWA, KAMON
APPLICANT: MATUSUE, TOMOKAZU
APPLICANT: NAGATA, SHIGEKAZU
                                                                                                                                                                                                                                                                                                                     STREET: Two Militia Dr
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
21P: 02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 96.0
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein
PCT-US95-05262-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 GTKLEI 126
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                                      121 GTKLEI 126
GTKLEI 126
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121
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61 DGTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MVSSAQFLGLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
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APPLICANT: CO, MAN SUNG
APPLICANT: VASQUEZ, MAXIMILIANO
TITLE OF INVENTION: ANTI-FAS LIGAND ANTI-FAS LIGAND ANTI-FAS LIGAND ANTI-FAS LIGAND ANTI-FAS LIGAND ANTI-FAS LIGAND ANTIBODY
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-458-516-5
; Sequence 5, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
    APPLICANT: Co, Man Sung
    APPLICANT: Tso, J. Yun
    TITLE OF INVENTION: Humanized Antibodies Reactive with
    TITLE OF INVENTION: GPIIB/IIIA
    NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
    ADDRESSEE: William M. Smith
    STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 127;
                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 22040-0747
ZIP: 22040-0747

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/649,100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 93.9%; Score 621; DB 3; Best Local Similarity 93.7%; Pred. No. 5.3e-57; Matches 118; Conservative 7; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1110-160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
ATORNEX/AGENT INFORMATION:
NAME: WIREHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
TELEFAX: (703) 205-8050
TELEFAX: (703) 205-8050
TELEFAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 127 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: One Market Pl
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS LENGTH: 127 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: peptide US-08-649-100-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 GTKLEI 126
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61 DGTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 DGTVKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIASYFCQQGYTPPWTFGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MVSSAQFLGLLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 92.6%; Score 612; DB 1; Length 127; Best Local Similarity 92.1%; Pred. No. 4.5e-56; Matches 116; Conservative 7; Mismatches 3; Indels
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Sequence 31.7

Sequen
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APPLICATION NUMBER: US/08/436,717
                                                                                                                                                                                                                                                                                                                                         53466/126/AAOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIF: 20007-5109
ZIF: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0,
                        PRIOR APPLICATION DATA.

APPLICATION NUMBER: JP 4-32084
FILING DATE: J9-FEB-1992
RHOR APPLICATION NUMBER: JP 3-95476
FILING DATE: S-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGINER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/12
TELECHONE: (202)672-5309
TELEPAN: C. (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 127 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein US-08-137-117D-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-436-717-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 DGIVKLLIYYTSTLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPWTFGG 120
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Patent No. 5795965
GENERAL.INFORMATION
APPLICANT: SATO. Koh
APPLICANT: BENDÍC, MATY
APPLICANT: SATO, Koh
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Mashington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 2007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILNG DATE: 20-DEC-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.6%; Score 619; DB 1; 92.9%; Pred. No. 8.5e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Mismatches
                                                                                                                                                                                     PLING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PREDICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 11823-37-3
REFERENCE/DOCKET NUMBER: 11823-37-3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-326-2402
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 92.9
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-08-458-516-5
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STATE: D
COUNTRY:
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61 DGTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: HANGEGAWA, MAMORU
APPLICANT: MASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: MIYAJI, HIROMASA
TILLE REPRENCE: 249-101
CURRENT APPLICATION NUMBER: US/09/225,322B
CURRENT FILING DATE: 1999-01-05
PRIOR PELICATION NUMBER: US 08/454,680
PRIOR PELICATION NUMBER: US 08/454,680
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR FILING DATE: 1995-05-31
PRIOR FILING DATE: 1995-05-31
PRIOR FILING DATE: 1995-09-17
PRIOR FILING DATE: 1994-08-17
PRIOR FILING DATE: 1994-08-17
PRIOR FILING DATE: 1994-08-17
PRIOR FILING DATE: 1994-09-17
PRIOR FILING DATE: 1991-09-18
PRIOR FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 10
SEQ ID NO 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
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Pred. No. 1.9e-55;
9; Mismatches 3;
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Pred. No. 3.9e-52;
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                                                                             MERCK 1743
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    ATTORNEY/AGENT INFORMATION:
NAME: Hamlet-King, Diana
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MER
TELECOMUNICATION:
TELECHONE: 703-243-6333
                                                                                                                                   INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 127 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 86.5%;
Matches 109; Conservative
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                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 90.5
Matches 114; Conservative
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -09-225-322B-10
                                                                                                                                                                                                                                                                                                                 US-08-574-699A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MVSTPQFLGLLLICFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MVSSAQFLGLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP 60
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APPLICANT: MITJANS, Francesc
APPLICANT: PIULATS, Jaune
APPLICANT: POSELL, Elisabet
APPLICANT: GOODMAN, Simon
APPLICANT: GOODMAN, Simon
APPLICANT: HAHN, Diane
ITILE OF INVENTION: Anti-alpha-V-Integrin Monoclonal
TITLE OF INVENTION: Antibody
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Millen, White, Zelano & Branigan, P.C.
STREET: Alington
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 22201

COMPUTER READABLE FORM:
MEDIUM TYPE Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PROCEDIATION
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/574,699A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92.6%; Score 612; DB 2;
92.1%; Pred. No. 4.5e-56;
tive 7; Mismatches 3;
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RIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94120165.9
FILING DATE: 20-DEC-1994
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/12
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08574699A
Patent No. 5985278
                                                                                                                                                                                                                                                                                                                                TELEX: 904136
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 92.1
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-08-436-717-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: #
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61 DGTIKLLIYYTSRLHSGVPSRFSGSGGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGG 120
                         61 DGTVKLLIFYSSNLHSGVPSRFSGGGGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGG 120
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                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: HANAL, NUBORO
APPLICANT: HASEGAMA, MAMORU
APPLICANT: HASEGAMA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUMANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT FILING DATE: 1999-01-05
PRIOR FILING DATE: 1995-05-31
PRIOR FILING DATE: 1995-05-31
PRIOR PLICATION NUMBER: US 08/454,680
PRIOR FILING DATE: 1995-03-21
PRIOR PLICATION NUMBER: US 08/408,133
PRIOR FILING DATE: 1995-03-21
PRIOR PLICATION NUMBER: US 08/292,178
PRIOR FILING DATE: 1995-09-17
PRIOR FILING DATE: 1992-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PRECENTION VOYET: 2.0
SEQ ID NO 19
LENGTH: 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MVSSAQFLGLLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
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Sequence 10, Application US/09764304
Sequence 10, Application US/09764304
Setent No. 6495666
GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, NAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUWANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence:light chain protest INFORMATION: variable region US-09-225-3228-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 128;
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                                                                                                                                                                                                                                                               Sequence 19, Application US/09225322B
Patent No. 6437098
PERERAL INFORMATION:
APPLICANT: SHITARA, KENYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                            121 GTKLEI 126
                                                                                                                                       121 GTKLEI 126
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US-09-225-322B-19
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61 DGTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGG 120
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Sequence 19, Application US/09764304
GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, MOBUO
APPLICANT: HANAI, MOBUO
APPLICANT: MINAJI, HIROMASA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT FILING DATE: 2010-10-19
CURRENT FILING DATE: 1999-01-05
EARLIER APPLICATION NUMBER: US 08/454,680
EARLIER PILING DATE: 1995-01-05
EARLIER PELING DATE: 1995-03-21
EARLIER PELING DATE: 1995-03-21
EARLIER PILING DATE: 1994-08-17
EARLIER PILING DATE: 1994-08-17
EARLIER FILING DATE: 1994-08-17
EARLIER PILING DATE: 1991-09-18
SARLIER PILING DATE: 1991-09-18
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                           CURRENT FILING DATE: 2001-01-09
EARLIER APPLICATION NUMBER: 09/225,322
EARLIER FILING DATE: 1995-01-05
EARLIER FILING DATE: 1995-01-05
EARLIER FILING DATE: 1995-05-31
EARLIER FILING DATE: 1995-05-31
EARLIER FILING DATE: 1995-05-31
EARLIER FILING DATE: 1995-03-21
EARLIER FILING DATE: 1995-03-17
EARLIER FILING DATE: 1994-08-17
EARLIER FILING DATE: 1994-08-17
EARLIER FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PARENTY NOWBER: JP 3-238375
EARLIER FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PARENTY NOWBER: JP 3-238375
EARLIER FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
APPLICATION NUMBER: US/09/764,304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: CDNA KM-641
US-09-764-304-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
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Length 127; Indels

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1 MVSSAQFLGLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
                   84.1%; Score 556; DB 3;
84.1%; Pred. No. 2.8e-50;
iive 10; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Lawrence, III, Stanton T
REGISTRATION UNDBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VETSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/434,122
FILING DATE: 05-NO. 6538111-1999
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/836,561
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: JP 232384/95
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear; ; MOLECULE TYPE: peptide; SEQUENCE DESCRIPTION: SEQ ID NO: 29: US-09-434-122-29
                                                                                                                                                                                                                                                                                                                                                                                               US-09-434-122-29; Application US/09434122; Sequence 29, Application US/09434122; Patent No. 6538111; GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 127 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: KOIKE, Masamichi
FURUYA, Akiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 29:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                     Query Match
Best Local Similarity 84.1<sup>3</sup>
Matches 106; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                              61 DGTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGG 120
                                                                                                                                                                                                                                                  1 MMSSAQFLGLLLLCFQGTRCDIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKP 60
                                                                                                                                                                                                           1 MVSSAQFLGLLLLCFQGTRCDIQMTQTTS$LSASLGDRVTISCRASQDISSYLNWYQQKP
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                                                                                                                         Length 128;
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TITLE OF INVENTION: Antibody Against Human Interleukin-5
TITLE OF INVENTION: Receptor Alpha Chain
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                  9; Indels
                                                                                                                         Score 574; DB 4;
Pred. No. 3.9e-52;
                                                                                                                                                                  8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEPHONE: 212-790-90741
TELERX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ...vresSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ Version 2.0
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,561
FILING DATE: 09-MX-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 09-MAY-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 232384/95
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FURUYA, Akiko
NAKAMURA, Kazuyasu
IIDA, Akihira
ANAZAWA, Hideharu
HANAI, NO. 6018032uo
                     ; FEATURE:
; OTHER INFORMATION: light chain
; OTHER INFORMATION: variable region
US-09-764-304-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 29, Application US/08836561
Patent No. 6018032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTR. 2
ZIP: 10036
COMPUTER READDABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                         86.8%;
86.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KOIKE, Masamichi
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 127 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                              GTKLEI 126
                                                                                                                                                                                                                                                                                                                                                                                                                   Grklei 126
                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: KOIKE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-836-561-29
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APPLICANT:
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                                                                                                                         Query Match
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61 DGTVELLIYHTSRLQSGVPSRFSGSGSGTDYSLTISDLEQEDIATYFCQQGYTLPYTVGG 120
61 DGTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGG 120
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                       84.1%; Score 556; DB 4; Length 127; 84.1%; Pred. No. 2.8e-50;
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0; Gaps
Matches 106; Conservative 10; Mismatches 10; Indels
                                                                                                            Search completed: October 22, 2003, 22:20:49 Job time : 14.4697 secs
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121 GTKLEI 126
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Tue Oct 28 10:01:49 2003
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Sequence 64, Appl
Sequence 5, Appli
Sequence 10, Appli
Sequence 10, Appl
Sequence 29, Appli
Sequence 29, Appli
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                                                                                                                                                                                October 22, 2003, 22:16:46; Search time 23.572 Seconds (without alignments) 902.237 Million cell updates/sec
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Sequence 2,
Sequence 1,
                                                                                                                                                                                                                                                                                                                                           661
1 MVSSAQFLGLLLCFQGTRC......CQQGNTLPYTFGGGTKLEIN 127
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1. (cgn2_6/prodata/2/pubpaa/USO7_PUBCOMB.pep:*

2. (cgn2_6/prodata/2/pubpaa/USO7_PUBCOMB.pep:*

3. (cgn2_6/prodata/2/pubpaa/USO6_PUBCOMB.pep:*

3. (cgn2_6/prodata/2/pubpaa/USO6_PUBCOMB.pep:*

5. (cgn2_6/prodata/2/pubpaa/USO6_PUBCOMB.pep:*

6. (cgn2_6/prodata/2/pubpaa/PCTUG_PUBCOMB.pep:*

7. (cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*

8. (cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*

10. (cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*

11. (cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*

12. (cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*

13. (cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*

13. (cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*

14. (cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*

15. (cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*

16. (cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*

17. (cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*

18. (cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*

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11. (cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*

12. (cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*

13. (cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*

14. (cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*

15. (cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*

16. (cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*

17. (cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*

18. (cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            629382
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-166-626-19
US-10-265-713-19
US-10-283-349-29
US-10-283-349-29
US-10-289-88-88
US-10-269-010-2
US-09-480-236-1
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2 US-10-268-883-5
5 US-10-084-139-2
US-09-764-304-10
US-09-764-304-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-779-784-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               629382 segs, 167460630 residues
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                              US-09-114-285A-29
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                              Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                  Seguence:
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                                                                                                                                                                                       Run on:
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Sequence 34, Appl Sequence 7, Appli Sequence 1, Appli Sequence 30, Appl Sequence 18, Appl	Sequence 3 Sequence 7 Sequence 1 Sequence 4 Sequence 9	10, 4, 21, 21, 21, 21, 21, 21, 21, 21, 21, 21	Sequence 21, Appl Sequence 6, Appli Sequence 73, Appl Sequence 73, Appl Sequence 71, Appl Sequence 71, Appl	Sequence 31 sequence 31 sequence 6, sequence 6, sequence 6, sequence 1, sequence 6, sequence 1,
2 US-10-310-674A 5 US-10-141-908- US-09-754-998-1 US-09-813-659-3 US-09-813-659-1 US-09-813-659-1	5 US-10-207-655-3 5 US-10-203-349-7 5 US-10-283-349-1 5 US-10-283-349-8 5 US-10-283-349-8	S US-10-283-349- US-09-056-160B- 2 US-10-234-671- 5 US-10-197-080- 1 US-09-929-665-	1 US-09-9259-546-2 1 US-09-9259-546-2 US-09-905-243-73 US-08-779-784-35 US-08-779-784-35 US-08-779-784-35	0-111-908- 0-141-908- 0-141-908- 0-859-053- 0-227-694-
107 108 108 1214 302 302 99	0000000	108 91 108 109 109 109 1109 1109 1109 11		233 233 233 233 233 233 233 233
523 79.1 517 78.2 512 77.5 512 77.5 512 77.5	2 77. 8 76. 5 76. 3 75.	744 . 73 . 73 . 73 . 73 . 73 . 73 . 73 .	,000000	144444 7777 1000 1000 1000
11 11 11 11 11 11 11 11	1 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0	22 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3		1 4 4 4 4 4 4 0 0 11 12 12 13 14 14 14 14 14 14 14 14 14 14 14 14 14

ALIGNMENTS

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Sequence 21, Application US/08779784
Publication No. US20020164325A1
GENERAL INFORMATION:
APPLICANT: Rodiguez, Noses
APPLICANT: Miller, David J.
APPLICANT: Asakura, Kunihiko
TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORFATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,784
FILING DATE: O7-JAN-1997
CLASSIFICATION NUMBER: US/08/79,784
PRIOR APPLICATION NUMBER: US/08/692,084
FILING DATE: 08-AUG-1996
PRIOR APPLICATION NUMBER: US/08/520
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                           ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza,
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
                                                                                                                                                                                                                                                                                                                                                                          CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
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Sequence 5, Application US/1026883

Sequence 5, Application US/1026883

Publication No. US2030138862A1

GENERAL INFORMATION:
APPLICANT: Green, Jennifer Macphate
TILE REFERENCE: 05802.0062.NPUS01

CURRENT APPLICATION NUMBER: US/10/268,883

CURRENT FILING DATE: 2003-03-26

PRIOR FILING DATE: 2001-10-10

PRIOR FILING DATE: 2001-11-21

NUMBER OF SEQ ID NOS: 16

SOFTWARE: Patentin Version 3.1

SEQ ID NOS: 16
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APPLICANT: YATOMI, Takehiro
APPLICANT: YATOMI, Takehiro
APPLICANT: SUDA, Takashi
TITLE OF INVENTION: PROPHYLACTIC/THERAPEUTIC AGENT
FILE REFERENCE: 1110-0307P
CURRENT APPLICATION NUMBER: US/10/084,139
CURRENT FILING DATE: 2002-12-09
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 2
LENGTH: 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 626; DB 12;
Pred. No. 1.9e-50;
7; Mismatches 1;
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ilarity 93.7%; Pred. No. 5.4e-50;
Conservative .7; Mismatches 1;
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Best Local Similarity 93.74
Matches 118; Conservative
                                                     121 GTKLEI 126
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                       121 GTKLEI 126
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Best Local Similarity
Matches 118; Conserv
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Sequence 64, Application US/10010729
Publication No. US20030185827A1
GENERAL INFORMATION:
APPLICANT: Redriguez, Moses
APPLICANT: Redriguez, Moses
APPLICANT: Miler, David J.
TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
FILE REPRENCE: 1199-1-005CIP2
CURRENT APPLICATION NUMBER: US/10/010,729
CURRENT APPLICATION NUMBER: US/130,473
PRIOR PRILING DATE: 2000-15-05
PRIOR APPLICATION NUMBER: 09/580,787
PRIOR APPLICATION NUMBER: 09/580,787
PRIOR APPLICATION NUMBER: 09/580,787
PRIOR APPLICATION NUMBER: 09/522,862
PRIOR APPLICATION NUMBER: 08/520
PRIOR APPLICATION NUMBER: 08/520
PRIOR APPLICATION NUMBER: 08/520
PRIOR FILING DATE: 1995-08-08
PRIOR FILING DATE: 1996-08-08
PRIOR FILING DATE: 1994-04-29
NUMBER OF SEQ ID NOS: 80
SOFTWARE: FRACESQ for Mindows Version 4.0
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                                                                                                                                                                                                                                                Length 131;
                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                       Score 638; DB 8;
Pred. No. 1.5e-51;
5; Mismatches 0,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                         TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                            Query Match
Best Local Similarity 96.0%;
Matches 121; Conservative
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Best Local Similarity 96.0
Matches 121; Conservative
                                                                                                                                                                           ) MOLECULE TYPE: protein US-08-779-784-21
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US-10-010-729-64
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US-10-010-729-64
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TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
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ORGANISM: Artificial Sequence
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                                                              61 DGTVKLLIYYTSRLHSGVPSRFSGSGSGTNYSLTISNLEQGDIATYFCQQGSTLPWTFGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                    GRENEAL INFORMATION:

APPLICANT: HANAI, NOBUO

APPLICANT: MYAJI, HIROWASA

TILE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY

FILE REFERENCE: 249-101

CURRENT APPLICATION NUMBER: US/09/764,304

CURRENT FILING DATE: 1999-01-05

EARLIER PILING DATE: 1999-01-05

EARLIER PILING DATE: 1999-01-05

EARLIER PILING DATE: 1995-05-31

EARLIER FILING DATE: 1995-03-21

EARLIER FILING DATE: 1995-03-21

EARLIER FILING DATE: 1995-09-17

EARLIER FILING DATE: 1991-09-18

SARLIER APPLICATION NUMBER: US 08/408,133

EARLIER FILING DATE: 1991-09-18

SARLIER PILING DATE: 1991-09-18

SOFTWARE: PAPENTICATION NUMBER: US 08/292,178

EARLIER PILING DATE: 1991-09-18

SOFTWARE: PAPENTICATION NUMBER: US 08/202,178

EARLIER PILING DATE: 1991-09-18

SOFTWARE: PAPENTICATION NUMBER: US 08/202,178

EARLIER FILING DATE: 1991-09-18

SOFTWARE: PAPENTICATION NUMBER: US 08/202,178

EARLIER FILING DATE: 1991-09-18

SOFTWARE: PAPENTICATION NUMBER: US 08/202,178

EARLIER FILING DATE: 1991-09-18

SOFTWARE: PAPENTICATION NUMBER: US 08/202,178

EARLIER FILING DATE: 1991-09-18

SOFTWARE: PAPENTICATION NUMBER: US 08/202,178

EARLIER FILING DATE: 1991-09-18

SOFTWARE: PAPENTICATION NUMBER: US 08/202,178

EARLIER FILING DATE: 1991-09-18

SOFTWARE: PAPENTICATION NUMBER: US 08/202,178

EARLIER FILING DATE: 1991-09-18

SOFTWARE: PAPENTICATION NUMBER: US 08/202,178
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Patent No. US20020026036A1
GENERAL INFORMATION:
APPLICANT: HANAI, NOBUO
APPLICANT: HARAII, NOBUO
APPLICANT: MIXAJI, HIROMASA
APPLICANT: MIXAJI, HIROMASA
APPLICANT: KUWANA, YOSHIHISA
                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/09764304
Patent No. US20020026036Al
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US-09-764-304-10
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US-09-764-304-19
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61 DGTVKLLIFYSSNIHSGVPSRFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGG 120
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| Publication No. US2003016876A1
| GENERAL INFORMATION:
| APPLICANT: SHIRARA KENYA
| APPLICANT: HANAI, NBUO
| APPLICANT: HASEGAWA, MAMORU
| APPLICANT: MIVALI, HIROMASA
| TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
| FILE REFERENCE: 249-101
| CURRENT APPLICATION NUMBER: US/09/225,322B
| PRIOR PILING DATE: 1995-06-12
| PRIOR FILING DATE: 1995-05-31
| PRIOR FILING DATE: 1995-05-31
| PRIOR FILING DATE: 1995-03-21
| PRIOR FILING DATE: 1995-09-17
| PRIOR FILING DATE: 1995-09-17
| PRIOR FILING DATE: 1994-09-17
| PRIOR FILING DATE: 1994-09-17
| PRIOR FILING DATE: 1995-09-17
| PRIOR FILING DATE: 1994-09-17
| PRIOR FILING DATE: 1994-09-18
| NUMBER OF SEQ ID NOS: 19
| SOFTWARE: PATENTIN VEY: 2.0
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CURRENT APPLICATION NUMBER: US/09/764,304
CURRENT FILING DATE: 2001-01-19
EARLIER APPLICATION NUMBER: US/09/764,304
EARLIER FILING DATE: 1999-01-05
EARLIER APPLICATION NUMBER: US 08/45,680
EARLIER APPLICATION NUMBER: US 08/45,680
EARLIER FILING DATE: 1995-05-31
EARLIER FILING DATE: 1995-05-31
EARLIER FILING DATE: 1994-08/17
EARLIER FILING DATE: 1991-09/17
EARLIER FILING DATE: 1991-09/17
EARLIER FILING DATE: 1991-09/17
EARLIER FILING DATE: 1991-09/17
EARLIER FILING DATE: 1991-09/18
NUMBER: OF SEQ ID NOS: 19
SEQ ID NOS: 19
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121 GTKLEI 126
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Sequence 19, Application US/10166626
Sequence 19, Application US/10166626
Sequence 19, Application US/10166876A1
GENERAL INFORMATION
APPLICANT: HANAI, NOBUO
APPLICANT: KUWANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT ELINGO BATE: 1090-010
CURRENT APPLICATION NUMBER: US/09/225,322B
PRIOR FILING DATE: 1999-01-05
PRIOR FILING DATE: 1999-01-05
PRIOR FILING DATE: 1999-01-01
PRIOR FILING DATE: 1999-03-1
PRIOR FILING DATE: 1999-03-1
PRIOR FILING DATE: 1999-09-1
PRIOR FILING DATE: 1999-09-1
PRIOR FILING DATE: 1999-09-17
PRIOR FILING DATE: 1999-09-17
PRIOR PLING DATE: 1999-09-17
PRIOR FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN VOIL 20
SEQ ID NO 19
LENGTH: 128
                                                                                                                                                                                                                    1 MVSSAQFLGLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
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                                                           ; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-166-626-10
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                                                                                                                                    Score 574; DB 12;
Pred. No. 1.2e-45;
8; Mismatches 9;
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Best Local Similarity 86.5%; Pred. No. 1.2e-45;
Matches 109; Conservative 8; Mismatches 9;
                  TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 86.5%;
Matches 109; Conservative
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61 DGTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGG 120
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FILE REPRENCE: 249-101.

CURRENT APPLICATION NUMBER: US/10/265,713

CURRENT FILING DATE: 2002-10-08

PRIOR PELING DATE: 1999-01-05

PRIOR PELING DATE: 1999-01-05

PRIOR APPLICATION NUMBER: US 08/454,680

PRIOR APPLICATION NUMBER: US 08/454,680

PRIOR APPLICATION NUMBER: US 08/408,133

PRIOR PELING DATE: 1995-03-1

PRIOR PILING DATE: 1994-08-17

PRIOR PILING DATE: 1994-08-17

PRIOR APPLICATION NUMBER: US 07/947,674

PRIOR APPLICATION NUMBER: US 08/292,178

PRIOR PILING DATE: 1991-09-18
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APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: HASEGAWA, MAMORU
APPLICANT: HIXAJ, HISANIA, YOSHIHISA
ITILE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/10/265,713
CURRENT FILING DATE: 2002-10-08
PRIOR APPLICATION NUMBER: US/09/225,322
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                                                                                                                                                                    Sequence 10, Application US/10265713; Publication No. US20030095964A1; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
121 GTKLEI 126
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61 DGTVELLIYHTSRLQSGVPSRFSGSGSGTDYSLTISDLEQEDIATYFCQQGYTLPYVGG 120
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Publication No. US20020127227A1
GENERAL INFORMATION:
APPLICANT: Julie A. Abrahamson
APPLICANT: Stephen D. Holmes
APPLICANT: Stephen D. Holmes
APPLICANT: Jeffrey R. Jackson
ITILE OF INVENTION: RHAMM Antagonist Antibodies
FILE REFERENCE: P50857
CURRENT FILING DATE: 2002-05-07
PRIOR PRICH OF THING DATE: 1999-11-19
PRIOR PELICATION NUMBER: US/09/443,790
PRIOR FILING DATE: 1999-11-19
PRIOR FILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.1%; Score 556; DB 15;
84.1%; Pred. No. 5.3e-44;
tive 10; Mismatches 10;
                                                                NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
APPLICATION NUMBER: JP 232384/95
                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFRAX: 212-869-9741
TELERX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acids
STRANDEDNESS: single
                     FILING DATE: 11-SEP-19
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 84.18
Matches 106; Conservative
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US-10-140-555-4
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US-10-140-555-4
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US-10-265-713-19
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FURUYA, Akiko
NAKAWURA, Kazuyasu
IIDA, Akihiro
ANAZAWA, Hideharu
HANAI, No. US20030096977Aluo
TAKATSU, Kiyosh
TAKATSU, Riyosh
Receptor Alpha Chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 128;
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Best Local Similarity 86.5%; Pred. No. 1.2e-45;
Matches 109; Conservative 8; Mismatches 9; Indels
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 29-Oct-2002
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION DATA:
APPLICATION NUMBER: US/08/836,561
FILING DATE: 09-MAY-1997
           PRIOR APPLICATION NUMBER: US 08/454,680
PRIOR FILING DATE: 1955-05-31
PRIOR APPLICATION NUMBER: US 08/408,133
PRIOR FILING DATE: 1955-03-21
PRIOR PILING DATE: 1954-08-17
PRIOR PILING DATE: 1994-08-17
PRIOR FILING DATE: 1992-09-17
PRIOR FILING DATE: 1992-09-17
PRIOR PILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 29, Application US/10283349 Publication No. US20030096977A1 GENERAL INFORMATION: APPLICANT: KOIKE, Masamichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
  FILING DATE: 1999-01-05
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| Publication No. US20030096285A1
| Publication No. US20030096285A1
| Publication No. US20030096285A1
| APPLICANT: Tso, Jonniffer
| TITLE OF INVENTION: NATI-HLA-DR ANTIBODIES AND THE METHODS OF USE THEREOF
| FILE REFERENCE: 05682.0062.NeUS01
| CURRENT APPLICATION NUMBER: US/10/269,010
| PRIOR FILING DATE: 2001-10-10
| PRIOR FILING DATE: 2001-10-11
| PRIOR FILING DATE: 2001-11-21
| NUMBER OF SEQ ID NOS: 2
| NUMBER OF SEQ ID NOS: 2
| CONTROL OF THE NOS: 3
| CONTROL OF THE NOS: 4
| CONTROL OF THE
                                                                                                                                            APPLICANT: TSO, J. Yun
APPLICANT: TSO, J. Yun
APPLICANT: Green, Jennifer Macphate
TITLE OF INVENTION: Anti-HLA-DR Antibodies and the Methods of Using Thereof
FILE REFERENCE: 05882.0062.NPUSB.
CURRENT APPLICATION NUMBER: US/10/268,883
CURRENT FILING DATE: 2003-303-26
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-11-21
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Version 3.1
ENGTH: 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGDTVPWTFGGGTKLEI 106
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Pred. No. 2.6e-41;
6; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.6%; Score 526; DB 12; 93.4%; Pred. No. 2.6e-41; iive 6; Mismatches 1;
                                 Sequence 6, Application US/10268883
Publication No. US20030138862A1
GENERAL INFORMATION:
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Best Local Similarity 93.4%;
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 93.4
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Mouse
US-10-268-883-6
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ORGANISM: Mouse
US-10-268-883-6
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USEQUENCE 1. Application US/09480236

Sequence 1. Application US/09480236

Fatent No. US20020142000A1

Sequence 1. Application US/09480236

Fatent No. US20020142000A1

SEDERATE INFORMATION:

APPLICANT: Digan, Mary Ellen

APPLICANT: Digan, Mary Ellen

TITLE OF INVENTION: Anti-CD3 Immunotoxins and Therapeutic Uses Therefor

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CURRENT APPLICATION NUMBER: US/09/480,236

CURRENT APPLICATION NUMBER: 22

SEQ ID NO 1

LENGTH: 601

SEQ ID NO 1

LENGTH: 601

SEQ ID NO 1

TYPE: FRT

ORGANISM: Artificial Sequence

CORGANISM: Artificial Sequence

SEC ID NO 1

LENGTH NEORMATION: ScFV (UCHT-1) - PE38 amino acid sequence

CORGANISM: Artificial Sequence

CORGANISM: Artificial Sequence

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CORGANISM: Artificial Sequence

SOFTHER INFORMATION: ScFV (UCHT-1) - PE38 amino acid sequence

CORGANISM: Artificial Sequence

SOFTHER INFORMATION: ScFV (UCHT-1) - PE38 amino acid sequence

CORGANISM: Artificial Sequence

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CORGANISM: Artificial Sequence

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SOFTHER INFO
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Search completed: October 22, 2003, 22:21:45 Job time: 24.572 secs